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OM protein - protein search, using sw model

Run on: December 27, 2005, 22:44:12 ; Search time 184 Seconds
(without alignments)
124.172 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGACRAGAPTIVL.....SSPARATLGKPLVLDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	268	100.0	52	2	AAY39293	Aay39293 CSA-1 cho
2	77	28.7	209	7	ABM87430	Abm87430 Rice abio
3	74	27.6	16	2	AAY39295	Aay39295 Polypepti
4	73.5	27.4	337	7	ADC32784	Adc32784 Human nov
5	73.5	27.4	675	9	AEA52600	Aea52600 Human Rab
6	73.5	27.4	791	5	ABP65089	Abp65089 Hypoxia-r
7	73.5	27.4	791	8	ADN03640	Adn03640 Antipsori
8	73.5	27.4	791	8	ADP22972	Adp22972 PRO polyp
9	73.5	27.4	863	6	ABP98856	Abp98856 Human str
10	73.5	27.4	863	7	ADC31071	Adc31071 Human nov
11	73.5	27.4	863	7	ADE48296	Ade48296 Human MIC
12	73.5	27.4	863	7	ADE48308	Ade48308 Human MIC
13	73.5	27.4	863	8	ABM82355	Abm82355 Tumour-as
14	72.5	27.1	173	7	ABO76575	Abo76575 Pseudomon
15	71.5	26.7	76	3	AAG28488	Aag28488 Zea mays
16	71	26.5	1938	6	ABP76682	Abp76682 Streptomy
17	69.5	25.9	210	4	AAU48625	Aau48625 Propionib
18	69.5	25.9	210	6	ABM45144	Abm45144 Propionib
19	68	25.4	315	5	ABU05772	Abu05772 M. tuberc
20	68	25.4	315	8	ABM79606	Abm79606 M tubercu
21	67.5	25.2	135	4	AAO01165	Aao01165 Human pol
22	67.5	25.2	137	7	ABO81794	Abo81794 Pseudomon
23	67	25.0	1321	9	ADV97797	Adv97797 Murine pr
24	66	24.6	228	7	ABO79635	Abo79635 Pseudomon

25	65.5	24.4	923	7	ADD18710	Add18710 Human dis
26	65.5	24.4	923	8	ADO19848	Ado19848 Human PRO
27	65.5	24.4	924	8	ADU06294	Adu06294 Novel bro
28	65	24.3	166	7	ABO68030	Abo68030 Pseudomon
29	65	24.3	205	7	ABO82421	Abo82421 Pseudomon
30	65	24.3	345	7	ABO77022	Abo77022 Pseudomon
31	64.5	24.1	146	7	ABO77184	Abo77184 Pseudomon
32	64.5	24.1	149	7	ABO82120	Abo82120 Pseudomon
33	64.5	24.1	309	4	ABG12975	Abg12975 Novel hum
34	64.5	24.1	341	8	ADK71091	Adk71091 Human MP2
35	64	23.9	137	3	AAG28496	Aag28496 Zea mays
36	63.5	23.7	223	8	ADY06811	Ady06811 Plant ful
37	63.5	23.7	377	9	ADY85271	Ady85271 Human ort
38	63.5	23.7	478	7	AAO30817	Aao30817 Human cel
39	63.5	23.7	721	7	ABO79547	Abo79547 Pseudomon
40	63	23.5	53	5	ABP01580	Abp01580 Human ORF
41	63	23.5	128	7	ADB64958	Adb64958 Human pro
42	63	23.5	128	7	ADM03909	Adm03909 Human pro
43	63	23.5	613	7	ABO71209	Abo71209 Pseudomon
44	63	23.5	1129	7	ABO73584	Abo73584 Pseudomon
45	62.5	23.3	85	4	AAU21041	Aau21041 Human nov

ALIGNMENTS

RESULT 1
AAY39293
ID AAY39293 standard; protein; 52 AA.

XX AC AAY39293;

XX DT 26-NOV-1999 (first entry)

XX DE CSA-1 chondrosarcoma associated protein-1.

XX KW Chondrosarcoma associated protein-1; CSA-1; bone malignancy; diagnosis;
XX KW rheumatoid arthritis; inflammatory arthropathy; tumour;
XX KW cartilage associated polypeptide; CAA-1.

XX OS Homo sapiens.

XX PN WO9946382-A1.

XX PD 16-SEP-1999.

XX PF 12-MAR-1999; 99WO-US005348.

XX PR 13-MAR-1998; 98US-00042225.

XX (RHOD-) RHODE ISLAND HOSPITAL LIFESPAN PARTNER.

XX Terek RM;

XX WPI; 1999-551411/46.

XX N-PSDB; AAZ06793.

XX New gene encoding a chondrosarcoma associated (CSA) polypeptide, useful
for diagnosing bone malignancy.

XX Claim 10; Page 18; 47pp; English.

XX This is the human chondrosarcoma associated protein-1 (CSA-1) amino acid
sequence. Chondrosarcoma is the second most common form of bone
malignancy and occurs in late adulthood and old age. CSA-1 is expressed
in a tumour cell line and also in some high grade chondrosarcoma, but not
in normal cartilage, or low or intermediate grade tumours. The CSA-1
polynucleotide and polypeptide can be used in methods and compositions
for evaluating appropriate treatment and treatment effectiveness of
malignancies associated with expression of CSA-1. CSA-1 polynucleotide
can be used as a probe to classify cells in terms of their level of CSA-1
expression or as primers for diagnostic PCR analysis in which mutations
and allelic variation of CSA-1 can be detected. Transgenic animals

PR 01-NOV-2002; 2002US-0423394P.
XX (GETH) GENENTECH INC.
PA
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR N-PSDB; ADP22971.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 7; SEQ ID NO 66; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bulous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 791 AA;
Query Match 27.4%; Score 73.5; DB 8; Length 791;
Best Local Similarity 45.7%; Pred. No. 1.9;
Matches 16; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTL-SHGSSSP 35
Db 516 SSGPQPAKPCSGATPTPLLLVGDRSPVSPGSSSP 550
RESULT 9
ABP98856
ID ABP98856 standard; protein; 863 AA.
XX
AC ABP98856;
XX
DT 15-JUL-2003 (first entry)
XX
DE Human structural and cytoskeletal associated protein #47.
XX
KW Cytostatic; antiarteriosclerotic; anticonvulsant; nootropic; antianginal;
KW neuroprotective; cerebroprotective; hypotensive; cardiant; osteopathic;
KW antiinflammatory; antiarthritic; virucide; gene therapy; human; stroke;
KW structural and cytoskeleton-associated protein; SCAP; cancer; angina;
KW atherosclerosis; epilepsy; Huntington's disease; hypertension;
KW heart failure; osteoporosis; osteoarthritis.
XX

OS Homo sapiens.
XX
PN WO2003031940-A2.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-US032851.
XX
PR 12-OCT-2001; 2001US-0328931P.
PR 19-OCT-2001; 2001US-0360681P.
PR 02-NOV-2001; 2001US-0343896P.
PR 09-NOV-2001; 2001US-0346308P.
PR 16-NOV-2001; 2001US-0332385P.
PR 07-DEC-2001; 2001US-0340776P.
PR 11-JAN-2002; 2002US-0347703P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Becha SD, Bhatia U, Blake JJ, Borowsky ML, Burrill JD, Chang H;
PI Chawla NK, Elliott VS, Emerling BM, Forsythe IJ, Gorvad AE;
PI Griffin JA, Hafalia AJA, Ho A, Ison CH, Kable AE, Khare R, Lal PG;
PI Lee S, Lee EA, Lee SY, Lehr-Mason PM, Li JX, Lindquist EA, Luo W;
PI Marquis JP, Ramkumar J, Richardson TW, Sprague WW, Swarnakar A;
PI Tang YT, Warren BA, Yang J, Yue H, Zebajadian Y, Zheng W;
XX
DR WPI; 2003-403125/38.
DR N-PSDB; ACC44343.
XX
PT New human structural and cytoskeleton-associated proteins (SCAP) useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant SCAP expression e.g. cancer, osteoporosis, or epilepsy.
XX
PS Claim 1; Page 303-305; 361pp; English.
XX
CC This sequence represents a novel isolated human structural and
CC cytoskeleton-associated protein (SCAP) polypeptide. The polypeptides and
CC polynucleotides encoding them are useful in diagnosing, treating and
CC preventing diseases or conditions associated with the decreased
CC expression or over expression of SCAP, such as cell proliferative (e.g.
CC cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's
CC disease, stroke), heart (e.g. hypertension, heart failure, angina) and
CC skeletal muscle disorders (e.g. osteoporosis, osteoarthritis) or viral
CC infections. These are also useful in assessing the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC SCAP. The SCAP or its fragments are useful in screening compounds for
CC effectiveness as agonist or antagonist of the polypeptides, or in
CC altering the expression of the target polynucleotide and compounds that
CC specifically bind to or modulate the activity of the polypeptide. The
CC microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles
XX
SQ Sequence 863 AA;
Query Match 27.4%; Score 73.5; DB 6; Length 863;
Best Local Similarity 45.7%; Pred. No. 2.1;
Matches 16; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTL-SHGSSSP 35
Db 588 SSGPQPAKPCSGATPTPLLLVGDRSPVSPGSSSP 622
RESULT 10
ADC31071
ID ADC31071 standard; protein; 863 AA.
XX
AC ADC31071;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel polypeptide sequence, SEQ ID NO:1153.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;

XX DE Human MICAL-1 like-protein.

XX KW MICAL domain; calponin homology domain; LIM domain; plexin;

XX KW Neuroprotective; Analgesic; Antiparkinsonian; Vulnerary; Tranquilizer;

XX KW Vasotropic; Cardiant; Nootropic; Gene therapy; Antisense gene therapy;

XX KW Cell therapy; Monooxygenase inhibitor; neurological condition.

OS Homo sapiens.

XX PN WO2003066821-A2.

XX PN 14-AUG-2003.

XX PF 04-FEB-2003; 2003WO-US003551.

XX PR 04-FEB-2002; 2002US-0354178P.

XX PR 30-MAY-2002; 2002US-0384302P.

XX PR 13-JUN-2002; 2002US-0388325P.

XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX X Kolodkin AL, Terman JR, Mao T, Pasterkamp RJ, Yu H;

XX WPI; 2003-731494/69.

XX N-PSDB; ADE48307.

XX New polypeptide comprising an N-terminal MICAL domain, a calponin

XX homology domain, a LIM domain, a proline rich region or a plexin

XX interacting region, useful for treating a neurological condition, e.g.,

XX Alzheimer's disease.

XX Claim 72; SEQ ID NO 14; 207pp; English.

XX The present sequence relates to an isolated polypeptide comprising an N-

XX terminal MICAL domain, a calponin homology domain, a LIM domain, a

XX proline rich region or a plexin interacting region, where the polypeptide

XX has monooxygenase activity. The polypeptide is useful for treating a

XX neurological condition, e.g., spinal cord injury, traumatic brain injury,

XX neuropathic pain, Parkinson's disease, Amyotrophic Lateral Sclerosis,

XX ischemic injury, Alzheimer's disease, multiple sclerosis or neuropathy

XX resulting from a stroke. The present sequence represents a MICAL protein.

XX Sequence 863 AA;

XX Query Match 27.4%; Score 73.5; DB 7; Length 863;

XX Best Local Similarity 45.7%; Pred. No. 2.1;

XX Matches 16; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTL-SHGSSSP 35

Db 588 SSGPQPAKPCSGATPTPLLLVGDSPVPSPGSSSP 622

RESULT 13

ABM82355

ID ABM82355 standard; protein; 863 AA.

XX ABM82355;

XX 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) polypeptide PRO83279, SEQ:6048.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX tumour; diagnosis; cell proliferative disorder; breast cancer;

XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;

XX central nervous system cancer; bladder cancer; pancreatic cancer;

XX cervical cancer; melanoma; leukaemia; hybridisation probe;

XX chromosome identification; chromosome mapping; gene mapping;

XX gene therapy; cytostatic.

XX Homo sapiens.

XX PN WO2004030615-A2.

XX PN 15-APR-2004.

XX PF 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN40936.

XX New tumor-associated antigenic target polypeptides and nucleic acids,

XX useful in preparing a medicament for treating or detecting a

XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or

XX prostate cancer or tumor.

XX Claim 12; SEQ ID NO 6048; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)

XX polypeptides, and their related nucleic acids. The TAT polypeptides are

XX overexpressed in cancer tissues compared to normal tissues, and may thus

XX serve as effective targets for the diagnosis and treatment of cancer in

XX mammals. The invention also relates to nucleic acid and polypeptide

XX sequences at least 80% identical to the TAT nucleic acids and

XX polypeptides; expression vectors and host cells comprising a TAT nucleic

XX acid; an antibody specific for a TAT polypeptide; a peptide or organic

XX molecule which binds to a TAT polypeptide; fusion proteins comprising a

XX TAT polypeptide; and methods and compositions for the treatment or

XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

XX antibodies, antagonists, binding molecules and compositions are useful

XX for diagnosing or treating a cell proliferative disorder associated with

XX increased TAT expression, particularly cancers such as breast cancer,

XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder

XX cancer, pancreatic cancer, cervical cancer, cancers of the central

XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be

XX used as hybridisation probes, in chromosome and gene mapping, in

XX chromosome identification and in gene therapy. The present sequence

XX represents a TAT polypeptide of the invention

XX Sequence 863 AA;

XX Query Match 27.4%; Score 73.5; DB 8; Length 863;

XX Best Local Similarity 45.7%; Pred. No. 2.1;

XX Matches 16; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTL-SHGSSSP 35

Db 588 SSGPQPAKPCSGATPTPLLLVGDSPVPSPGSSSP 622

RESULT 14

ABO76575

ID ABO76575 standard; protein; 173 AA.

XX ABO76575;

XX 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polypeptide #8750.

XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX Pseudomonas aeruginosa.

XX US6551795-B1.

XX 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
DR N-PSDB; ABD10146.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 25321; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 173 AA;

Query Match 27.1%; Score 72.5; DB 7; Length 173;
Best Local Similarity 40.5%; Pred. No. 0.41;
Matches 17; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

Qy 5 PRPGAPCRAGAPTIVLTSGRRQTLSHG---SSSPARATLGKP 43
||| ||||| | : ||: | : ||| | |
Db 44 PRPARACRAGAGTDTATGAARRRFRAGAGPRRAGTPTRAPAGSP 85

RESULT 15
AAG28488
ID AAG28488 standard; protein; 76 AA.
XX
AC AAG28488;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 33724.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR

PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR

PR	19-JUL-1999;	99US-0144325P;
PR	19-JUL-1999;	99US-0144331P;
PR	19-JUL-1999;	99US-0144332P;
PR	19-JUL-1999;	99US-0144333P;
PR	19-JUL-1999;	99US-0144334P;
PR	19-JUL-1999;	99US-0144335P;
PR	20-JUL-1999;	99US-0144352P;
PR	20-JUL-1999;	99US-01444632P;
PR	20-JUL-1999;	99US-01444884P;
PR	21-JUL-1999;	99US-0144814P;
PR	21-JUL-1999;	99US-0145086P;
PR	21-JUL-1999;	99US-0145088P;
PR	22-JUL-1999;	99US-0145085P;
PR	22-JUL-1999;	99US-0145087P;
PR	22-JUL-1999;	99US-0145089P;
PR	22-JUL-1999;	99US-0145192P;
PR	23-JUL-1999;	99US-0145145P;
PR	23-JUL-1999;	99US-0145218P;
PR	23-JUL-1999;	99US-0145224P;
PR	26-JUL-1999;	99US-0145276P;
PR	27-JUL-1999;	99US-0145913P;
PR	27-JUL-1999;	99US-0145918P;
PR	27-JUL-1999;	99US-0145919P;
PR	28-JUL-1999;	99US-0145951P;
PR	02-AUG-1999;	99US-0146386P;
PR	02-AUG-1999;	99US-0146388P;
PR	02-AUG-1999;	99US-0146389P;
PR	03-AUG-1999;	99US-0147038P;
PR	04-AUG-1999;	99US-0147204P;
PR	04-AUG-1999;	99US-0147302P;
PR	05-AUG-1999;	99US-0147192P;
PR	05-AUG-1999;	99US-0147260P;
PR	06-AUG-1999;	99US-0147303P;
PR	06-AUG-1999;	99US-0147416P;
PR	09-AUG-1999;	99US-0147493P;
PR	09-AUG-1999;	99US-0147935P;
PR	10-AUG-1999;	99US-0148171P;
PR	11-AUG-1999;	99US-0148319P;
PR	12-AUG-1999;	99US-0148341P;
PR	13-AUG-1999;	99US-0148565P;
PR	13-AUG-1999;	99US-0148684P;
PR	16-AUG-1999;	99US-0149368P;
PR	17-AUG-1999;	99US-0149175P;
PR	18-AUG-1999;	99US-0149426P;
PR	20-AUG-1999;	99US-0149722P;
PR	20-AUG-1999;	99US-0149723P;
PR	20-AUG-1999;	99US-0149929P;
PR	23-AUG-1999;	99US-0149902P;
PR	23-AUG-1999;	99US-0149930P;
PR	25-AUG-1999;	99US-0150566P;
PR	26-AUG-1999;	99US-0150884P;
PR	27-AUG-1999;	99US-0151065P;
PR	27-AUG-1999;	99US-0151066P;
PR	27-AUG-1999;	99US-0151080P;
PR	30-AUG-1999;	99US-0151303P;
PR	31-AUG-1999;	99US-0151438P;
PR	01-SEP-1999;	99US-0151930P;
PR	07-SEP-1999;	99US-0152363P;
PR	10-SEP-1999;	99US-0153070P;
PR	13-SEP-1999;	99US-0153758P;
PR	15-SEP-1999;	99US-0154018P;
PR	16-SEP-1999;	99US-0154039P;
PR	20-SEP-1999;	99US-0154779P;
PR	22-SEP-1999;	99US-0155139P;
PR	23-SEP-1999;	99US-0155486P;
PR	24-SEP-1999;	99US-0155659P;
PR	28-SEP-1999;	99US-0156458P;
PR	29-SEP-1999;	99US-0156596P;
PR	04-OCT-1999;	99US-0157117P;
PR	05-OCT-1999;	99US-0157753P;
PR	06-OCT-1999;	99US-0157865P;
PR	07-OCT-1999;	99US-0158029P;
PR	08-OCT-1999;	99US-0158232P;

XX The invention relates to avilamycin derivatives (I) with antibacterial,
CC virucide, protozoacide and fungicide activity. (I) are useful for
CC treatment of infections (bacterial, viral, protozoal or fungal), in human
CC or veterinary medicine, particularly where caused by Staphylococcus
CC aureus. (I) are more hydrophilic than known avilamycins. The present
CC sequence is that of an avilamycin synthesis enzyme from the Streptomyces
CC viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
CC ABZ37516)
XX
SQ Sequence 19938 AA;

polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations or antigen-presenting cells that express the
CC polypeptides are useful for diagnosing, preventing or treating acne
CC vulgaris, or for stimulating an immune response specific for a P. acnes
CC protein. The polynucleotides can also be used as probes or primers for
CC nucleic acid hybridisation. The vaccine composition is useful for the
CC stimulation of an immune response against P. acnes, or for treating acne,
CC and the kit is useful for performing a diagnostic assay. The present
CC sequence represents a polypeptide predicted to be encoded by an ORF (open
CC reading frame) contained within the P. acnes polynucleotides of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 210 AA;

Query Match 25.9%; Score 69.5; DB 6; Length 210;
Best Local Similarity 38.3%; Pred. No. 1.3;
Matches 18; Conservative 5; Mismatches 19; Indels 5; Gaps 2;

QY 2 AAGPRPGAPCRAGAPTIVL-----TSGRRQTLSHGSSSPARA-TLGKP 43
Db 85 AVHPRHGCPTRGRSVVAVSREDSRGRSRTAPHGHRPARSRLGVP 131

RESULT 19
ABU05772
ID ABU05772 standard; protein; 315 AA.

XX AC ABU05772;
XX DT 08-APR-2003 (first entry)
XX DE M. tuberculosis and M. leprae marker protein #423.
XX KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
XX KW mycobacterial disease; tuberculosis; leprosy.
OS Mycobacterium tuberculosis.
OS Mycobacterium leprae.

XX PN WO200274903-A2.
XX PD 26-SEP-2002.
XX PF 22-FEB-2002; 2002WO-IB001973.
XX PR 22-FEB-2001; 2001US-0270123P.
XX PA (INSP) INST PASTEUR.
XX PI Cole S;
XX DR WPI; 2002-759885/82.

XX PT Identifying and selecting genes for survival or virulence of mycobacteria
XX PT by a comparative genomic analysis of the sequences of Mycobacterium
XX PT tuberculosis and M. leprae.
XX PS Claim 17; Page 623-624; 874pp; English.

XX CC This invention relates to a novel method for identifying essential genes
XX CC for survival or virulence of mycobacteria species. The method comprises
XX CC aligning the genomic sequence of a first mycobacterium species on a
XX CC genomic sequence of a second mycobacterium species and selecting a
XX CC polynucleotide sequence that is highly conserved in both genomes with no
XX CC counterparts in other bacterial genomic sequences and that corresponds to
XX CC an essential gene for the survival or virulence of mycobacterium species.
XX CC The method of the invention is useful for detecting M. tuberculosis or M.
XX CC leprae infection. The method reduces the number of potential new targets
XX CC and protective antigens for new drugs and vaccine compositions to treat
XX CC and prevent mycobacterial diseases, particularly tuberculosis and
XX CC leprosy. The present sequence represents a marker protein from

CC Mycobacterium tuberculosis and Mycobacterium leprae identified using the
CC method of the invention
XX SQ Sequence 315 AA;
Query Match 25.4%; Score 68; DB 5; Length 315;
Best Local Similarity 28.2%; Pred. No. 3.4;
Matches 20; Conservative 5; Mismatches 14; Indels 32; Gaps 2;

QY 1 MAAGPRPGAPC-----RAGAPT-----IVLTSGRRQTL 28
Db 51 LVAGSRPGGPPIGYLNLSPPRGAGGAMAEVLVHPQSRRRRGIGTAMARAALAKTAGRNQFW 110

QY 29 SHGSSSPARAT 39
Db 111 AHGTLDPARAT 121

RESULT 20
ABM79606
ID ABM79606 standard; protein; 315 AA.
XX AC ABM79606;
XX DT 22-APR-2004 (first entry)
XX DE M tuberculosis MshD protein.
XX KW Enzyme; mycothiol synthesis; MshC; MshD; MshA; infection;
XX KW cysteine:glucosaminyl inositol ligase; antibacterial;
XX KW acetyl-CoA:Cys-GlcN-Ins acetyltransferase.
OS Mycobacterium tuberculosis.
XX PN WO2003089585-A2.
XX PD 30-OCT-2003.
XX PF 15-APR-2003; 2003WO-US011539.
XX PR 15-APR-2002; 2002US-0373079P.
XX PR 19-APR-2002; 2002US-0373890P.
XX PA (REGC) UNIV CALIFORNIA.
XX PA (UYBR-) UNIV BRITISH COLUMBIA.
XX PI Sareen D, Newton GL, Fahey RC, Buchmeier N, Steffek M, Av-Gay Y;
XX PI Rawat M, Koledin T;
XX DR WPI; 2004-042359/04.

XX PT Identifying inhibitors of mycothiol biosynthesis, useful as antibacterial
XX PT agents and for increasing sensitivity to antibiotics, also mycothiol-
XX PT defective mutant actinomycetes.
XX PS Claim 38; Fig 10A; Opp; English.

XX CC The present invention relates to a method for identifying an inhibitor of
XX CC cysteine:glucosaminyl inositol ligase (CGIL), which comprises treating
XX CC test compound with such a ligase in presence of a cysteine and a
XX CC glucosaminyl inositol, or their derivatives and determining if ligation
XX CC of cysteine and glucosaminyl inositol has occurred. Agents which inhibit
XX CC cysteine:glucosaminyl inositol ligase, or other enzymes involved in
XX CC biosynthesis of mycothiol (MSH), are used to reduce virulence, increase
XX CC antibiotic sensitivity and inhibit growth of MSH-producing bacteria,
XX CC especially for treatment of infections by Mycobacterium species, but also
XX CC e.g. Corynebacterium diphtheriae or Actinomyces israelii. New mutant
XX CC forms of actinomycetes that have mutated MSH-synthesis genes and can only
XX CC survive briefly in white blood cells are useful as vaccines. The present
XX CC sequence is a polypeptide which is/forms part of an enzyme relevant to
XX CC the invention

XX SQ Sequence 315 AA;

DT 15-JAN-2004 (first entry)
XX Human disease related protein SeqID141.
DE human; disease state; cytostatic; antiinflammatory; ophthalmological;
XX antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX Homo sapiens.
OS WO2003018621-A2.
PN 06-MAR-2003.
XX 23-AUG-2002; 2002WO-GB003892.
PD 23-AUG-2001; 2001GB-00020558.
PF 05-OCT-2001; 2001GB-00024037.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX WPI; 2003-290046/28.
DR N-PSDB; ADD18711.
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX Claim 25; SEQ ID NO 141; 424pp; English.
PS This invention relates to novel human genes and gene product which are
XX implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnery activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX Sequence 923 AA;
SQ Query Match 24.4%; Score 65.5; DB 7; Length 923;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 7; Indels 9; Gaps 1;
QY 3 AGPRPGAPCRAGPTIVLTSGRRQTLSHGSSSPAR 37
Db ||| ||||| |: |:| |:|
45 AGPARACPCRAGTPS-----TMSSPASTPSR 70
RESULT 26
ADO19848
ID ADO19848 standard; protein; 923 AA.
XX ADO19848;
XX 12-AUG-2004 (first entry)
DT Human PRO polypeptide #386.
DE

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX Homo sapiens.
OS WO2004043361-A2.
XX 27-MAY-2004.
PN 06-NOV-2003; 2003WO-US035268.
PD 08-NOV-2002; 2002US-0425235P.
PF (GETH) GENENTECH INC.
XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
XX WPI; 2004-420067/39.
DR N-PSDB; ADOI9847.
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX Claim 7; SEQ ID NO 772; 1731pp; English.
PS The invention relates to human PRO polypeptides and the polynucleotides
XX encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.
XX Sequence 923 AA;
SQ Query Match 24.4%; Score 65.5; DB 8; Length 923;
Best Local Similarity 40.0%; Pred. No. 26;
Matches 14; Conservative 5; Mismatches 7; Indels 9; Gaps 1;
QY 3 AGPRPGAPCRAGPTIVLTSGRRQTLSHGSSSPAR 37
Db ||| ||||| |: |:| |:|
45 AGPARACPCRAGTPS-----TMSSPASTPSR 70
RESULT 27
ADU06294
ID ADU06294 standard; protein; 924 AA.
XX ADU06294;
XX 27-JAN-2005 (first entry)
DT Novel bronchial cancer-associated human protein SeqID518.
XX bronchial cancer; cytostatic; tumour-associated protein;
KW cancer detection; metastasis; tumour; human.
XX Homo sapiens.
OS

CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 146 AA;

Query Match 24.1%; Score 64.5; DB 7; Length 146;
Best Local Similarity 35.4%; Pred. No. 3.9;
Matches 17; Conservative 5; Mismatches 19; Indels 7; Gaps 1;

QY 3 AGPRGAPCRAGAPTIVLTSGRRQTLSHGS-----SSPARATLGKP 43
| | | | | : | | | | : | | | | : | | | | :
DB 8 ASPRSGSPMTAGRWSIPMGSGTRSTATSSPPAGYSRSPSTAVASP 55

RESULT 32
ABO82120
ID ABO82120 standard; protein; 149 AA.
XX
AC ABO82120;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #14295.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX

PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD15691.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 30866; 455pp; English.
XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

SQ Sequence 149 AA;
Query Match 24.1%; Score 64.5; DB 7; Length 149;
Best Local Similarity 41.7%; Pred. No. 3.9;

Matches 15; Conservative 2; Mismatches 10; Indels 9; Gaps 1;
QY 4 GPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARAT 39
| | | | | : | | | | : | | | | : | | | | :
DB 99 GARPGGSCR-----NGRRQSGHAWGSPQRAS 125

RESULT 33
ABG12975
ID ABG12975 standard; protein; 309 AA.
XX
AC ABG12975;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #12956.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS77162.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX

PS Claim 20; SEQ ID NO 43334; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 309 AA;
Query Match 24.1%; Score 64.5; DB 4; Length 309;
Best Local Similarity 34.0%; Pred. No. 9.5;
Matches 17; Conservative 11; Mismatches 13; Indels 9; Gaps 2;

KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX Unidentified.
OS US2004034888-A1.
XX
PN 19-FEB-2004.
XX
PD 28-APR-2003; 2003US-00425114.
XX
PF 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
PR
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 62626; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 223 AA;

Query Match 23.7%; Score 63.5; DB 8; Length 223;
Best Local Similarity 34.8%; Pred. No. 8.7;
Matches 16; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY 2 AAGPRPGAPCR-AGAPTIVLTSGRRQTLSHGSSSPARATLKGKPLVL 46
:|||||:| :|||:| :|||:| :|||:| :|||:|
Db 106 SAGPRPSSTSRPPWAAAAAARARRRLLPRGAASPRRRRARRPLL 151

RESULT 37
ADY85271
ID ADY85271 standard; protein; 377 AA.
XX
AC ADY85271;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human orthologue of CD4.4 gene-encoded protein.
XX
KW Cell cycle; restenosis; vasotropic; cardiovascular disease; neoplasm;

KW lymphoma; lung tumor; colon tumor; ovary tumor; cytostatic;
KW RNA interference; gene silencing; antibody therapy; drug screening;
KW CD4.4.
XX
OS Homo sapiens.
XX
PN WO2005026359-A2.
XX
PD 24-MAR-2005.
XX
PF 15-SEP-2004; 2004WO-EP010307.
XX
PR 15-SEP-2003; 2003US-0502633P.
XX
PA (CENI-) CENIX BIOSCIENCE GMBH.
XX
XX Echeverri C, Hyman A, Goenczy P, Soennichsen B, Jones S, Walsh A;
PI Koski L;
PI
XX
DR WPI; 2005-233496/24.
DR N-PSDB; ADY85270.
DR GENBANK; CAD38936.
XX
PT Use of a nucleic acid molecule, polypeptide, or an antibody directed
PT against the polypeptide, for manufacturing a medicament that inhibits or
PT activates spindle formation or microtubule function during cell division.
XX
PS Claim 8; SEQ ID NO 36; 184pp; English.
XX
CC The invention relates to the functional role of several Caenorhabditis
CC elegans genes and of their corresponding gene products in spindle
CC formation or microtubule formation during cell division that can be
CC identified by means of RNA interference (RNAi), and to the identification
CC and isolation of functional orthologues of these genes and their
CC biologically functional derivatives. The invention also relates to the
CC use of these genes and gene products, including the orthologues, in the
CC development or isolation of anti-proliferative agents, particularly their
CC use in screening assays, and their use for diagnosis and treatment of
CC proliferative and other diseases. In particular, the invention relates to
CC the use of small interfering RNAs (siRNAs) derived from the genes for the
CC treatment of proliferative diseases. The proliferative disease is
CC especially coronary restenosis or a neoplastic disease selected from
CC lymphoma, lung cancer, colon cancer, ovarian cancer and breast cancer
CC (all claimed). The present sequence is that of the human orthologue of
CC the C. elegans CD4.4 protein ADY85267. Characterization of the nematode
CC gene by RNAi indicated a requirement for CD4.4 gene function in spindle
CC formation or microtubule formation during cell division. Based on the
CC extremely high sequence conservation at the protein level, these
CC functions are probably also found in humans. The use of a polypeptide
CC having the present sequence for the manufacture of a medicament for the
CC inhibition of spindle formation or microtubule formation during cell
CC division is claimed.
XX
SQ Sequence 377 AA;

Query Match 23.7%; Score 63.5; DB 9; Length 377;
Best Local Similarity 40.5%; Pred. No. 16;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;

QY 5 PR---PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLKGK 43
||| ||| ||| ||| : ||| : ||| |||
Db 290 PRPGYPTPMGASGPGYPLRGGRAFPSPGYPQQSPYPATGGKP 331

RESULT 38
AAO30817
ID AAO30817 standard; protein; 478 AA.
XX
AC AAO30817;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human cell adhesion and extracellular matrix protein (CADECM) -7.

XX Human; cell adhesion and extracellular matrix protein; immune disorder;
KW CADECM; cancer; gene therapy.
XX Homo sapiens.
XX WO2003047526-A2.
XX
PD 12-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038437.
XX
PR 30-NOV-2001; 2001US-0334343P.
PR 07-DEC-2001; 2001US-0340278P.
PR 04-JAN-2002; 2002US-0345069P.
PR 25-JAN-2002; 2002US-0351352P.
PR 14-FEB-2002; 2002US-0357168P.
PR 29-MAR-2002; 2002US-0369128P.
PR 05-APR-2002; 2002US-0370802P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Baughn MR, Becha SD, Bhatia U, Blake JJ, Borowsky ML, Burrill JD;
PI Delegeane AM, Elliott VS, Gandhi AR, Gietzen KJ, Gorvad AE;
PI Griffin JA, Ho A, Jin P, Kable AE, Lal PG, Lee EA, Lee S, Lee SY;
PI Marquis JP, Lehr-Mason PM, Ramkumar J, Richardson TW, Sprague WW;
PI Swarnakar A, Tang TY, Tran B, Tran UK, Chawla NK, Warren BA, Xu Y;
PI Yue H, Zheng W;
XX
DR WPI; 2003-513695/48.
DR N-PSDB; AAL62019.
XX
PT New human cell adhesion and extracellular matrix proteins (CADECM)
PT polypeptide, useful for preparing a composition for treating a disease
PT associated with decreased expression or overexpression of CADECM e.g.,
PT cancer.
XX
PS Claim 1; Page 279-280; 374pp; English.
XX
XX The invention relates to human cell adhesion and extracellular matrix
CC proteins (CADECM) and nucleic acid molecules encoding such proteins.
CC CADECM proteins are useful for preparing a composition for diagnosing or
CC treating a disease or condition associated with decreased expression or
CC overexpression of functional CADECM e.g., immune disorders or cancer. The
CC invention is also useful in gene therapy. The present sequence is human
CC CADECM protein
XX
SQ Sequence 478 AA;

Query Match 23.7%; Score 63.5; DB 7; Length 478;
Best Local Similarity 40.5%; Pred. No. 22;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;

QY 5 PR---PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
Db ||||| : : : : :
268 PRPGYPGTPMGASGPGYPLRGGRAPSPGYPQQSPYPATGGKP 309

RESULT 39
ABO79547
ID ABO79547 standard; protein; 721 AA.
XX
AC ABO79547;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #11722.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX Pseudomonas aeruginosa.
OS
XX US6551795-B1.

XX 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD13118.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 28293; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 721 AA;

Query Match 23.7%; Score 63.5; DB 7; Length 721;
Best Local Similarity 36.8%; Pred. No. 36;
Matches 21; Conservative 4; Mismatches 17; Indels 15; Gaps 2;

QY 4 GPRP-----GAPCRAGAPTIVLTSGRRQTLSHG-----SSSPARATLGKPLV 45
Db ||||| : : : : :
242 GRRPDPQAGAPCTARATTGRAGSGRRLTSRPGCRRWRTCGRPANAAACRRSLGSPSV 298

RESULT 40
ABP01580
ID ABP01580 standard; protein; 53 AA.
XX
AC ABP01580;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:3142.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US010836.
PF 30-MAY-2000; 2000US-0206132P.
XX 29-AUG-2000; 2000US-0228716P.
PR (CURA-) CURAGEN CORP.
XX Shimkets RA, Leach MD;
PI WPI; 2002-106308/14.
DR N-PSDB; ABN17332.
DR Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
PT
XX Disclosure; SEQ ID NO 3142; 1037pp; English.
PS
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 53 AA;
Query Match 23.5%; Score 63; DB 5; Length 53;
Best Local Similarity 33.3%; Pred. No. 1.8;
Matches 15; Conservative 4; Mismatches 16; Indels 10; Gaps 1;
QY 10 PCRAGAPTIVLTSGRRQTLSHGSS-----PARATLGKPL 44
Db 3 PLRVGTPTGALTANRHVSKRSTASRRGRGVAPEPAHTTRGRPV 47
RESULT 41
ADB64958
ID ADB64958 standard; protein; 128 AA.
XX
AC ADB64958;
XX
XX 04-DEC-2003 (first entry)
DT Human protein encoded by clone PROST20058860.
XX
XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
OS Homo sapiens.
XX EP1308459-A2.
PN

XX 07-MAY-2003.
PD 28-MAR-2002; 2002EP-00007401.
XX 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-450961/43.
DR N-PSDB; ADB62988.
DR New polynucleotides and polypeptides, useful for developing a diagnostic
XX marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
PT
XX Claim 1; Page; 222pp; English.
PS The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 128 AA;
Query Match 23.5%; Score 63; DB 7; Length 128;
Best Local Similarity 35.6%; Pred. No. 5.2;
Matches 16; Conservative 4; Mismatches 23; Indels 2; Gaps 1;
QY 4 GPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVIND 48
Db 2 GPAGHAAPRGPPVPATTAG--AALRAGASEPQTQLGAPLALGE 44
RESULT 42
ADM03909
ID ADM03909 standard; protein; 128 AA.
XX
AC ADM03909;
XX
XX 20-MAY-2004 (first entry)
DT Human protein of the invention SEQ ID NO:2594.
XX human; gene therapy; diagnostic marker; pharmaceutical.
KW
XX Homo sapiens.
OS

XX EPI347046-A1.
PN
XX
PD 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
PF
XX
PR 22-MAR-2002; 2002JP-00137785.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM01466.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
PS Claim 1; SEQ ID NO 2594; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.
XX
SQ Sequence 128 AA;

Query Match 23.5%; Score 63; DB 7; Length 128;
Best Local Similarity 35.6%; Pred. No. 5.2;
Matches 16; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY 4 GPRGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVIND 48
Db 2 GPAAGHAAPRGPPVPATTAG--AALRAGASEPRQTQLGAPLALGE 44

RESULT 43
ABO71209
ID ABO71209 standard; protein; 613 AA.
XX
AC ABO71209;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #3384.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX

DR WPI; 2003-615309/58.
DR N-PSDB; ABD04780.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 19955; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 613 AA;

Query Match 23.5%; Score 63; DB 7; Length 613;
Best Local Similarity 41.0%; Pred. No. 34;
Matches 16; Conservative 5; Mismatches 16; Indels 2; Gaps 1;

QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
Db 165 PRPGADPRGPARQAARIAGRHR--AHGPSANPDAPLGRP 201

RESULT 44
ABO73584
ID ABO73584 standard; protein; 1129 AA.
XX
AC ABO73584;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #5759.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR N-PSDB; ABD07155.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 22330; 455pp; English.
XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1129 AA;

Query Match 23.5%; Score 63; DB 7; Length 1129;
Best Local Similarity 44.8%; Pred. No. 72;
Matches 13; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 13 AGAPTIVLTSGRRQTLSHGSSSPARATLG 41
 :|:|:| | | | | | | | | | | | | | | |
Db 938 SGSGLVLASGARIDLRHGTAAPAEQVDG 966

RESULT 45
AAU21041
ID AAU21041 standard; protein; 85 AA.
XX
AC AAU21041;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human novel foetal antigen, SEQ ID NO 1285.
XX
KW Human; foetal tissue antigen; antiinflammatory; neuroprotective;
KW immunomodulator; cardiovascular; cytostatic; nephrothropic;
KW cardiovascular; autoimmune disease; rheumatoid arthritis;
KW hyperproliferative disorder; breast neoplasm; cancer;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; food additive.

XX Homo sapiens.

XX WO200155312-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001321.

PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-488782/53.
DR N-PSDB; AAS33861.
XX

PT New polynucleotides and polypeptides for diagnosing, treating, preventing
PT or prognosing e.g. diseases or disorders of the nervous, musculoskeletal,
PT excretory, gastrointestinal, reproductive, and respiratory systems.

XX Claim 11; SEQ ID NO 1285; 642pp; English.

XX
CC The invention relates to novel nucleic acids encoding novel human foetal
CC antigens. The nucleic acids and proteins are used to prevent, treat (e.g.
CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. The antibodies to the antigens can also be used
CC in alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection.

CC The polypeptides can also be used to aid wound healing and epithelial
CC cell proliferation, to prevent skin aging due to sunburn, to maintain
CC organs before transplantation, for supporting cell culture of primary
CC tissues, to regenerate tissues and in chemotaxis. The polypeptides can
CC also be used as a food additive or preservative to increase or decrease
CC storage capabilities, fat content, lipid, protein, carbohydrate,
CC vitamins, minerals, cofactors and other nutritional components. Numerous
CC examples of diseases and disorders treated by the nucleic acids and
CC proteins are given in the specification. The present sequence represents
CC a foetal antigen of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained

Query Match 23.3%; Score 62.5; DB 4; Length 85;
Best Local Similarity 40.4%; Pred. No. 3.7;
Matches 19; Conservative 1; Mismatches 16; Indels 11; Gaps 2;

QY 3 AGPRP-GAPCRAGAPTIVLTSGRRQ-----TLSHGSSSPARA 38
||| | | | | | | | | | | | | | | | | | | | | |
Db 28 AGPRANGVPCNWGVGLDVLGVREQQPPTGTCERGTGVSSHGSEQPARA 74

Search completed: December 27, 2005, 23:00:26
Job time : 188 secs

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Db 437 APAQAGDPS---TQSRHPSMHGSSHPS 461

|| :|| | : | | | | |||| | :

RESULT 22

S24390

transforming protein (Bcl-2) homolog - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004

C;Accession: S24390

R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.

Biochim. Biophys. Acta 1132, 109-113, 1992

A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue

A;Reference number: S24390; MUID:92379084; PMID:1511008

A;Accession: S24390

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-232 <CAZ>

A;Cross-references: UNIPROT:Q00709; UNIPARC:UPI000017124D; EMBL:Z11961; NID:g62969; PIDN

C;Superfamily: Bcl2 related apoptosis regulator

C;Keywords: mitochondrion; transmembrane protein

Query Match 20.9%; Score 56; DB 2; Length 232;

Best Local Similarity 41.9%; Pred. No. 35;

Matches 18; Conservative 2; Mismatches 17; Indels 6; Gaps 2;

Qy 2 AAG-PRPGACRAGPTIVLTSGRRQTLSHGSSSPARATL 40

||| | | | | | | | | : | | | | |

Db 31 AAGEDRPVPFPAPAPAAAPAAVAAG--ASSHRPSPPARLLL 71

RESULT 23

T46420

hypothetical protein DKFZp434M1123.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46420

R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A;Reference number: Z23034

A;Accession: T46420

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-430 <AAA>

A;Cross-references: UNIPROT:Q9NT83; UNIPARC:UPI00000706EA; EMBL:AL137478

A;Experimental source: adult testis; clone DKFZp434M1123

C;Genetics:

A;Note: DKFZp434M1123.1

Query Match 20.9%; Score 56; DB 2; Length 430;

Best Local Similarity 35.3%; Pred. No. 65;

Matches 12; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Qy 7 PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATL 40

| | | | | : : | | | | | : | |

Db 138 PADPCEGARSCLVTESARGGLQNGQSVDEETL 171

RESULT 24

S21825

vicilin-like storage protein Glb1-S, embryo - maize

C;Species: Zea mays (maize)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S21825

R;Kriz, A.L.

submitted to the EMBL Data Library, April 1991

A;Reference number: S21823

A;Accession: S21825

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-540 <KRI>

A;Cross-references: UNIPROT:Q03866; UNIPARC:UPI000000A6C7D; EMBL:X59084; NID:g22285; PIDN

C;Genetics:

A;Gene: Glb1-S

A;Introns: 170/1; 195/2; 222/2; 319/2

C;Superfamily: glycinin

Query Match 20.9%; Score 56; DB 2; Length 540;

Best Local Similarity 47.6%; Pred. No. 82;

Matches 20; Conservative 1; Mismatches 15; Indels 6; Gaps 3;

Qy 2 AAGPRPGAPCR----AGAPTIVLTSGRRQTLSHGSSS-PARA 38

|| | | | | | | | | | | | | | |

Db 260 AATARTG-PCRRSASRAAPTASWTSGPASPTSTGSSSTRPTRA 300

RESULT 25

A72627

probable 2-oxoacid-ferredoxin oxidoreductase, alpha chain APE1473 - Aeropyrum pernix (st;

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: A72627

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki

DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: A72627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-616 <XAW>

A;Cross-references: UNIPROT:Q9YBX7; UNIPARC:UPI000005DF74; DDBJ:AP0000061; NID:g5104821; I

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE1473

C;Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid fer

F;227-409/Domain: 2-oxoacid ferredoxin oxidoreductase homology <FEO>

Query Match 20.9%; Score 56; DB 2; Length 616;

Best Local Similarity 40.5%; Pred. No. 94;

Matches 15; Conservative 0; Mismatches 8; Indels 14; Gaps 1;

Qy 1 MAAGPRPGAPCRAG-----APTIVLTSG 23

| | | | | | | | | | | | | | |

Db 329 MRAGPSTGMPTRTGQQDLLHSIFSGHGDPKIVLASG 365

RESULT 26

F84470

probable retroelement pol polyprotein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: F84470

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: F84470

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-780 <STO>

A;Cross-references: UNIPROT:Q9SL06; UNIPARC:UPI000009D1F1; GB:AE002093; NID:g4581164; PII

C;Genetics:

A;Gene: At2g05610

A;Map position: 2

Query Match 20.9%; Score 56; DB 2; Length 780;

Best Local Similarity 35.3%; Pred. No. 1.2e+02;

Matches 12; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 14 GAPTIVLTSGRR---QTLSHGSSSPARATLTKP 43

| | : : | | | | | : | |

Db 602 GCPSSIVSSRRVLVQHQLSHSTWTPYEA VYGP 635

QY	5	PRPG-APCRGAPTIVLTSGRRQTLSHGS-----SSPARATLGKPLVLND---YSLN 52
		: : : : :
Db	713	PSPSTAPSASADPAMEPLTTERNTESHGDAAASPEPLSSPAH-TLNSEVVFNEDSTYILN 771
		:
RESULT 31		
A40996		phenylalanine 4-monooxygenase (EC 1.14.16.1) - Chromobacterium violaceum
N;Alternate names:		phenylalaninase; phenylalanine 4-hydroxylase
C;Species:		Chromobacterium violaceum
C;Date:		03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 09-Jul-2004
C;Accession:		A40996; B40996
R;Onishi, A.;		Liotta, L.J.; Benkovic, S.J.
J. Biol. Chem.		266, 18454-18459, 1991
A;Title:		Cloning and expression of Chromobacterium violaceum phenylalanine hydroxylase i
A;Reference number:		A40996; MUID:92011593; PMID:1655752
A;Accession:		A40996
A;Molecule type:		DNA
A;Residues:		1-296 <ONI>
A;Cross-references:		UNIPROT:P30967; UNIPARC:UPI000016EBD9; GB:M55915; NID:g144481; PIDN:
A;Accession:		B40996
A;Molecule type:		protein
A;Residues:		1-20 <ONS>
A;Cross-references:		UNIPARC:UPI0000017AA1E
A;Experimental source:		strain ATCC 12540
C;Keywords:		biopterin; oxidoreductase
Query Match		20.5%; Score 55; DB 2; Length 296;
Best Local Similarity		38.9%; Pred. No. 59;
Matches		14; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
QY	12	RAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVLN 47
		: : : :
Db	254	RAGFRSAILAAGRRATVGRGDIAP-----DDLVLN 283
		: : : :
RESULT 32		
C86384		unknown protein [imported] - Arabidopsis thaliana
C;Species:		Arabidopsis thaliana (mouse-ear cress)
C;Date:		02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession:		C86384
R;Theologis, A.;		Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.;		Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.;		Hughes, B.; Huizar, L.
Nature		408, 816-820, 2000
A;Authors:		Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.;		Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.;		Rooney, T.; Rowley, D.; Sakano, H.
A;Authors:		Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.;		Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title:		Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number:		A86141; MUID:21016719; PMID:11130712
A;Accession:		C86384
A;Status:		preliminary
A;Molecule type:		DNA
A;Residues:		1-323 <STO>
A;Cross-references:		UNIPROT:Q9C6L2; UNIPARC:UPI00000AC544; GB:AE005172; NID:g10092333; F
C;Genetics:		
A;Map position:		1
Query Match		20.5%; Score 55; DB 2; Length 323;
Best Local Similarity		32.6%; Pred. No. 64;
Matches		15; Conservative 8; Mismatches 15; Indels 8; Gaps 1;
QY	1	MAAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVL 46
		: : : : : :
Db	285	LASADRATAAARAAALV-----NVSYGATTPTVAEGKPLNL 322
		: : : : : :
RESULT 33		
JC2466		inhibin beta-C chain precursor - human

N;Alternate names:		activin beta C chain
C;Species:		Homo sapiens (man)
C;Date:		29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession:		JC2466
R;Hoetten, G.;		Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun.		206, 608-613, 1995
A;Title:		Cloning of a new member of the TGF-beta family: A putative new activin betaC ch
A;Reference number:		JC2466; MUID:95126961; PMID:7826378
A;Accession:		JC2466
A;Molecule type:		mRNA
A;Residues:		1-352 <HOE>
A;Cross-references:		UNIPROT:P55103; UNIPARC:UPI000012D42A; GB:X82540; NID:g669154; PIDN:(
A;Experimental source:		liver
C;Genetics:		
A;Gene:		GDB:INHBC
A;Cross-references:		GDB:632884
A;Map position:		2cen-2ql3
C;Superfamily:		inhibin
C;Keywords:		glycoprotein
F;1-18/Domain:		signal sequence #status predicted <SIG>
F;19-236/Domain:		propeptide #status predicted <PRO>
F;237-352/Product:		activin beta C #status predicted <MAT>
F;110,143,161/Binding site:		carbohydrate (Asn) (covalent) #status predicted
Query Match		20.5%; Score 55; DB 2; Length 352;
Best Local Similarity		36.0%; Pred. No. 70;
Matches		18; Conservative 3; Mismatches 21; Indels 8; Gaps 2;
QY	3	AGRRPGAPCRA-GAPTIVLTSGRRQTLSHGSS-----PARATLGKPL 44
Db	18	ATPRAGGQCPACGGPTLELSQRELLLDLAKRSILDKLHLTQRPPTLNRPV 67
RESULT 34		
TVHUML		transforming protein L-myc-1 - human
C;Species:		Homo sapiens (man)
C;Date:		30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession:		A27675; S01200; S09390
R;Kaye, F.;		Battey, J.; Nau, M.; Brooks, B.; Seifter, E.; De Greve, J.; Birrer, M.; Sausa
Mol. Cell. Biol.		8, 186-195, 1988
A;Title:		Structure and expression of the human L-myc gene reveal a complex pattern of alt
A;Reference number:		A27675; MUID:88094386; PMID:2827002
A;Accession:		A27675
A;Molecule type:		DNA
A;Residues:		1-364 <KAY>
A;Cross-references:		UNIPROT:P12524; UNIPARC:UPI0000012FAF3; GB:M19720; NID:g188906; PIDN:1
R;Depinho, R.A.;		Hatton, K.S.; Testaye, A.; Yancopoulos, G.D.; Alt, F.W.
Genes Dev.		1, 1311-1326, 1987
A;Title:		The human myc gene family: structure and activity of L-myc and an L-myc pseudoge
A;Reference number:		S01200; MUID:88112807; PMID:3322939
A;Accession:		S01200
A;Molecule type:		DNA
A;Residues:		1-364 <DEP>
A;Cross-references:		UNIPARC:UPI0000012FAF3
R; Ikegaki, N.;		Minna, J.; Kennett, R.H.
EMBO J.		8, 1793-1799, 1989
A;Title:		The human L-myc gene is expressed as two forms of protein in small cell lung ca
A;Reference number:		S09390; MUID:89356654; PMID:2548855
A;Accession:		S09390
A;Status:		preliminary
A;Molecule type:		protein
A;Residues:		165-179 <IKE>
A;Cross-references:		UNIPARC:UPI000001732D0
C;Genetics:		
A;Gene:		GDB:MYCL1
A;Cross-references:		GDB:120706; OMIM:164850
A;Map position:		1p32-1p32
A;Introns:		166/1
C;Superfamily:		myc transforming protein; myc transforming protein homology
C;Keywords:		DNA binding; nucleus; transforming protein
F;1-364/Domain:		myc transforming protein homology <MYC>

Query Match 20.5%; Score 55; DB 1; Length 364;
Best Local Similarity 31.1%; Pred. No. 72;
Matches 19; Conservative 5; Mismatches 13; Indels 24; Gaps 4;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPA-----RATLG--KPLV 45
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 137 AGNPAPAAPCPPLGEP-----KTQACS-GSESPSDSENEEIDVVTVVEKRSQSLGIRKPVT 188
46 L 46
189 I 189

RESULT 35
E87561
hypothetical protein CC2518 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87561
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87561
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-445 <STO>
A;Cross-references: UNIPROT:Q9A5D2; UNIPARC:UPI00000C7762; GB:AE005673; NID:g13424075; F
C;Genetics:
A;Gene: CC2518

Query Match 20.5%; Score 55; DB 2; Length 445;
Best Local Similarity 43.2%; Pred. No. 88;
Matches 19; Conservative 3; Mismatches 18; Indels 4; Gaps 2;

QY 1 MAAGPRPGAPCRAG---APTIVLTSGRRQTLSHGSSSPARATLG 41
: | | | | | : | | | | : | | | | : | | | | : | | | | :
Db 252 LGAGPFDEAAATGVQQAARMITLLAQGRQTFINGWSSP-RANLG 294

RESULT 36
G84263
long-chain fatty-acid-CoA ligase [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84263
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithäuser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <STO>
A;Cross-references: UNIPROT:Q9HQH8; UNIPARC:UPI00000637E1; GB:AE004437; NID:g10580623; F
C;Genetics:
A;Gene: lf11
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 20.5%; Score 55; DB 2; Length 493;
Best Local Similarity 34.0%; Pred. No. 98;
Matches 18; Conservative 7; Mismatches 12; Indels 16; Gaps 4;

QY 8 GAP-----CRAGAPTIVLTSGRRQTL-----HGSSSPAR-ATLGKPLV 45
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 268 GAPTPELVERACAAGVP-VCPTYGATETASQAATLHASDAPAHPESVGRPLL 319

RESULT 37
AD1959
ATP-dependent RNA helicase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD1959
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-513 <KUR>
A;Cross-references: UNIPROT:Q8YXJ0; UNIPARC:UPI00000CE00E; GB:EA000019; PIDN:BA07180.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1223

Query Match 20.5%; Score 55; DB 2; Length 513;
Best Local Similarity 40.6%; Pred. No. 1e+02;
Matches 13; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

QY 12 RAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 479 RRGTPPKPLRTGRRET---SATPSNPKLGGSP 506

RESULT 38
E70722
hypothetical protein Rv1836c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70722
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70722
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-677 <COL>
A;Cross-references: UNIPROT:Q50597; UNIPARC:UPI000013B324; GB:Z78020; GB:AL123456; NID:g
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv1836c
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1788.28

Query Match 20.5%; Score 55; DB 2; Length 677;
Best Local Similarity 38.1%; Pred. No. 1.4e+02;
Matches 16; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
| | | | | : | | | | : | | | | : | | | | : | | | | :
Db 317 AASAPAGAPATAGIGAVRTLMGARPKLADDSLTAAAMDTLKP 358

RESULT 39
A55523
hypothetical protein (bphD 3' region) - Pseudomonas sp. (strain KKS102)
C;Species: Pseudomonas sp.
C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 11-Jan-2002
C;Accession: A55523
R;Kikuchi, Y.; Nagata, Y.; Hinata, M.; Kimbara, K.; Fukuda, M.; Yano, K.; Takagi, M.
J. Bacteriol. 176, 1689-1694, 1994
A;Title: Identification of the bphA4 gene encoding ferredoxin reductase involved in biphe
A;Reference number: A55523; MUID:94179104; PMID:8132464
A;Accession: A55523

A;Accession: C64841
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-848 <BLAT>
A;Cross-references: UNIPROT:P33225; UNIPARC:UPI0000137173; GB:AE000201; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
R;Mejean, V.; Iobbi-Nivol, C.; Lepelletier, M.; Giordano, G.; Chippaux, M.; Pascal, M.C.
Mol. Microbiol. 11, 1169-1179, 1994
A;Title: TMAO anaerobic respiration in Escherichia coli: involvement of the tor operon.
A;Reference number: S43697; MUID:94293785; PMID:8022286
A;Accession: S43698
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172, 'R', 174-175, 'R', 177-255, 'R', 257, 'S', 259-280, 'G', 282-324, 'E', 326-347, 'S'
A;Cross-references: UNIPARC:UPI000016F536; EMBL:X73888; NID:g556701; PIDN:CAA52095.1; PI
A;Experimental source: strain K-12
C;Genetics:

A;Gene: torA
C;Function:
A;Description: reduces trimethylamine-N-oxide into trimethylamine
C;Superfamily: trimethylamine-N-oxide reductase
C;Keywords: molybdenum; NAD; oxidoreductase; periplasmic space
F;1-39/Domain: signal sequence #status predicted <SIG>
F;40-848/Product: trimethylamine-N-oxide reductase #status predicted <MAT>

Query Match 20.3%; Score 54.5; DB 2; Length 848;
Best Local Similarity 36.1%; Pred. No. 1.9e+02;
Matches 13; Conservative 6; Mismatches 10; Indels 7; Gaps 1;

Qy 4 GERPAPCRAGAPTIVLTSGRRQTLSHGSSSPARAT 39
Db 778 GGEFGALCKYGNPNVL-----TIDIGTSQLAQAT 806

RESULT 45
T30717
probable virion protein 115L - Mollusum contagiosum virus 1
N;Alternate names: MC115L
C;Species: Mollusum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30717
R;Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: Z20876; MUID:96325459; PMID:8670425
A;Accession: T30717
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-178 <SEN>
A;Cross-references: UNIPROT:Q98282; UNIPARC:UPI00000F6094; EMBL:U60315; NID:g1491943; PI
C;Genetics:
A;Note: MC115L
C;Superfamily: vaccinia virus 20K virion protein

Query Match 20.1%; Score 54; DB 2; Length 178;
Best Local Similarity 29.4%; Pred. No. 46;
Matches 15; Conservative 10; Mismatches 22; Indels 4; Gaps 2;

Qy 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVINDYSLN 52
Db 132 SSSPRPRAP-RSGTTR---STGTRSSGARSRGSPRRRATGDSPSMPDYGMD 178

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Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium;
Mycobacterium tuberculosis complex.
NCBI_TaxID=1765;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garner T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248336; CAD93704.1; -; Genomic_DNA.
HSSP; O53831; 1POH.
SMR; Q7U173; 3-310.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl trans.
DR Pfam; PF00583; Acetyltransf_1; 2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 315 AA; 33599 MW; E1728C0652CF2716 CRC64;

Query Match 25.4%; Score 68; DB 2; Length 315;
Best Local Similarity 28.2%; Pred. No. 12;
Matches 20; Conservative 5; Mismatches 14; Indels 32; Gaps 2;

QY 1 MAAGPRPGAPC-----RAGAPT-----IVLTSGRRQTL 28
Db 51 LVAGSRPGGPIIGYLNLSPPRGAGGAMAELVVHPQSRRRGIGTAMARAALAKTAGRNQFW 110

QY 29 SHGSSSPARAT 39
Db 111 AHGTLDPARAT 121

RESULT 8
O53831_MYCTU
ID O53831_MYCTU PRELIMINARY; PRT; 315 AA.
AC O53831; Q7D982;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MT0841, Rv0819;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
NUCLEOTIDE SEQUENCE.
STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
RN [2]
NUCLEOTIDE SEQUENCE.
STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,

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Db 211 KAGADMRSRG---IITSGSRNTLIHGGSSNRRRLRGDPV 246

RESULT 10

ID Q4UVP4_XANCP PRELIMINARY; PRT; 563 AA.
AC Q4UVP4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE N-acetylmuramoyl-L-alanine amidase.
GN ORFNames=XC_1816;
OS Xanthomonas campestris pv. campestris str. 8004.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=314565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8004;
RA Qian W., Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F.,
RA Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,
RA Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tian Y.-C., Yao Z.-J., Fu G.,
RA Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
RA He C.-Z.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000050; AAY48879.1; -; Genomic DNA.
SQ SEQUENCE 563 AA; 57271 MW; 5860B59189C35941 CRC64;

Query Match 25.0%; Score 67; DB 2; Length 563;
Best Local Similarity 46.9%; Pred. No. 31;
Matches 15; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPA 36

Db 229 PRPGTVAAPGAP--ATTGGTRTTIATGTPSPA 258

RESULT 11

ID Q8P8E3_XANCP PRELIMINARY; PRT; 563 AA.
AC Q8P8E3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE N-acetylmuramoyl-L-alanine amidase.
GN Name=amiC;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Fortmighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012337; AAM41578.1; -; Genomic DNA.

DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3_hydro.
DR Pfam; PF01520; Amidase_3; 1.
DR SMART; SM00646; Ami_3; 1.
KW Complete proteome.
SQ SEQUENCE 563 AA; 57270 MW; 5860B59189C35941 CRC64;

Query Match 25.0%; Score 67; DB 2; Length 563;
Best Local Similarity 46.9%; Pred. No. 31;
Matches 15; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPA 36

Db 229 PRPGTVAAPGAP--ATTGGTRTTIATGTPSPA 258

RESULT 12

ID Q9M4X9_CHLRE PRELIMINARY; PRT; 1787 AA.
AC Q9M4X9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Flagellar autotomy protein Falp.
GN Name=FAL;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20267878; PubMed=10806107;
RA Finst R.J., Kim P.J., Griffis E.R., Quarmby L.M.;
RT "Falp is a 171 kDa protein essential for axonemal microtubule severing
RT in Chlamydomonas.";
RL J. Cell Sci. 113:1963-1971(2000).
DR EMBL; AF246990; AAF66419.1; -; mRNA.
DR HSSP; P37595; 1JN9.
DR GO; GO:0019861; C:flagellum; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007091; LRR_RNinh.
DR Pfam; PF00560; LRR_1; 1.
DR PRINTS; PR01590; HTHFIS.
KW Flagellum; Leucine-rich repeat; Repeat.
SQ SEQUENCE 1787 AA; 171585 MW; 452A74259EE14DC1 CRC64;

Query Match 24.8%; Score 66.5; DB 2; Length 1787;
Best Local Similarity 38.6%; Pred. No. 1.3e+02;
Matches 22; Conservative 4; Mismatches 14; Indels 17; Gaps 3;

QY 2 AAG-----PRPGAPCRAGAPTIVL-----TSGRRQTL-----SHGSSSPARATLG 41

Db 230 AAGGSAPRPGTAGAGPATAVLGGSGGLMPPGQQSLPLSGPSASSSQPGAVTLG 286

RESULT 13

ID Q743X3_MYCPA PRELIMINARY; PRT; 272 AA.
AC Q743X3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP0468;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;

[1]
NUCLEOTIDE SEQUENCE.
STRAIN=k10;
Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AE017228; AAS02785.1; -; Genomic DNA.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR000073; A/b_hydrolase.
InterPro; IPR000379; Ser_estr.
PFam; PF00561; Abhydrolase_1; 1.
Complete proteome; Hydrolase.
SEQUENCE 272 AA; 30094 MW; 07DB5A382CC8B749 CRC64;

Query Match 24.6%; Score 66; DB 2; Length 272;
Best Local Similarity 40.4%; Pred. No. 18;
Matches 19; Conservative 2; Mismatches 8; Indels 18; Gaps 3;

QY 4 GPRPGAPCR-----AGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVL 46
||||| | | | | | | | | | | | | | | | | | | | | |
Db 7 GPRPGQPARCTQDGMFSTVLT-----RHGGH-----GEPLVL 39

RESULT 14
Q8IV50 HUMAN
ID Q8IV50_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q8IV50;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Hypothetical protein MGC35274 (Putative peptidoglycan binding domain
DE protein-like protein).
GN Name=MGC35274;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Ding P., Han W., Wang Y., Rui M., Chen Y., Wang L., Ma D.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC033515; AAH33515.1; -; mRNA.
EMBL; AY125955; AAM94507.1; -; mRNA.
DR Ensembl; ENSG00000140280; Homo sapiens.

DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR InterPro; IPR002482; LysM.
DR Pfam; PF01476; LysM; 1.
DR SMART; SM00257; LysM; 1.
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23463 MW; A87E666478E903AC CRC64;

Query Match 24.1%; Score 64.5; DB 2; Length 215;
Best Local Similarity 34.0%; Pred. No. 21;
Matches 17; Conservative 11; Mismatches 13; Indels 9; Gaps 2;

QY 5 PRPGAP-----CRAGAPT-----IVLTSGRRQTLSHGSSSPARATLGKPLV 45
||||| | | | | | | | | | | | | | | | | | | | | |
Db 18 PRPSAPSPPPRRSRSGSEEAELSLSLARTKTRSYGSTASVRAPLGAGVI 67

RESULT 15
Q82NB1 STRAW
ID Q82NB1_STRAW PRELIMINARY; PRT; 596 AA.
AC Q82NB1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative transcriptional regulator.
GN OrderedLocusNames=SAVL392;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RC MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531 (2003).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RC MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).
DR EMBL; BA000030; BAC69102.1; -; Genomic DNA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR002078; Sig54_interact.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF02954; HTH_8; 1.
DR Pfam; PF00158; Sigma54_activat; 1.
DR PRINTS; PR01590; HTHFIS.
DR TIGRFAMs; TIGR01199; HTH_fis; 1.
DR PROSITE; PS50045; SIGMA54_INTERACT_4; 1.
KW Complete proteome.
SQ SEQUENCE 596 AA; 65277 MW; ADEE4EAAE22DF77D CRC64;

Query Match 24.1%; Score 64.5; DB 2; Length 596;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 18; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 11 CR-----AGAPTIVLTSGRRQTLSHGSSSPARATLG 41
||||| | | | | | | | | | | | | | | | | | | | | |
Db 288 CRREDSADAGAVFRVRLIGRLQPTSGSASPARSSLG 323

RESULT 16
Q4WQ64_ASPFU PRELIMINARY; PRT; 613 AA.
AC Q4WQ64;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Phosphatidyl synthase.
GN ORFNames=Afu4g11720;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA Penalva M.A., Perteaux S., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000005; EAL89620.1; -; Genomic DNA.
SQ SEQUENCE 613 AA; 67112 MW; CB87DA382B769C4F CRC64;

Query Match 23.9%; Score 64; DB 2; Length 613;
Best Local Similarity 39.5%; Pred. No. 78;
Matches 15; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 16 PTIVLTSGRRQTLSHGSSSPARATLG--KPLVLNDYSL 51
Db 13 PTAIPLVGPKEGLDAGSAVPGRITMSLVLPFIIGNYSL 50

RESULT 17
Q4Q5C4_LEIMA PRELIMINARY; PRT; 731 AA.
AC Q4Q5C4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF32.1570;
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; CT005269; CAJ08678.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 731 AA; 79723 MW; 20FDD7282CBEA2EB CRC64;

Query Match 23.9%; Score 64; DB 2; Length 731;
Best Local Similarity 35.3%; Pred. No. 95;
Matches 18; Conservative 2; Mismatches 31; Indels 0; Gaps 0;

QY 2 AAGPRPGACRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVLNDYSLN 52
Db 287 AGGPEAAAPALANTPGVAEESGVNSTRRRTAKRANKTTTAPPVLLDEMLN 337

RESULT 18
Q5R9T2_PONPY PRELIMINARY; PRT; 355 AA.
ID Q5R9T2_PONPY PRELIMINARY;
AC Q5R9T2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp468H155.
GN Name=DKFZp468H155;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Ansorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR859300; CAH91478.1; -; mRNA.
DR InterPro; IPR009851; Mod_r.
DR Pfam; PF07200; Mod_r; 1.
KW Hypothetical protein.
SQ SEQUENCE 355 AA; 38393 MW; 1BF12B70E94C5788 CRC64;

Query Match 23.7%; Score 63.5; DB 2; Length 355;
Best Local Similarity 40.5%; Pred. No. 48;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;

QY 5 PR---PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
Db 268 PRPGYPTGTGASGPGYPLAGRALSPGYQQSPYPATGKGP 309

RESULT 19
Q8N3K4_HUMAN PRELIMINARY; PRT; 377 AA.
ID Q8N3K4_HUMAN PRELIMINARY;
AC Q8N3K4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp761I097 (Fragment).
GN Name=DKFZp761I097;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Amnigdala;
RA Koehler K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834261; CAD38936.1; -; mRNA.
DR Ensembl; ENSG00000167987; Homo sapiens.
DR InterPro; IPR009851; Mod_r.
DR Pfam; PF07200; Mod_r; 1.
KW Hypothetical protein.

FT NON TER 1 1
SQ SEQUENCE 377 AA; 41650 MW; 0EBDFCFF524A4CD6 CRC64;
Query Match 23.7%; Score 63.5; DB 2; Length 377;
Best Local Similarity 40.5%; Pred. No. 51;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;
QY 5 PR---PGAPCRAGAPTIVLTSGRRQTLTSHGSSSPARATLGKP 43
Db 290 PRPGYPGTPMGASGPGYPLRGGRAPSPGYPQQSPYPATGGKP 331
RESULT 20
Q8BQZ7_MOUSE
ID Q8BQZ7_MOUSE PRELIMINARY; PRT; 562 AA.
AC Q8BQZ7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230338M15 product:DEAD/H (Asp-Glu-Ala-
DE Asp/His) box polypeptide 26, full insert sequence. (Fragment).
GN Name=Ddx26;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Fujita M., Gariboldi M.,
RA Brownstein M.J., Bult C., Fletcher C., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Tomita M., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK046055; BAC32584.1; -; mRNA.
DR MGI; MGI:1202397; Ddx26.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000629; DEAD box.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; UNKNOWN_1.
FT NON TER 1 1
SQ SEQUENCE 562 AA; 64142 MW; 233C3BCEEA51D4A7 CRC64;
Query Match 23.7%; Score 63.5; DB 2; Length 562;
Best Local Similarity 37.7%; Pred. No. 81;
Matches 23; Conservative 2; Mismatches 21; Indels 15; Gaps 4;
QY 3 AGP-----RPGAPCRAGAP-----TIVLTSGRRQT---LSH--GSSSPARATLGKPLVLN 47
Db 324 AGPQNKHKRPGEPSMQGIPKRRRCASPLLRGRQSPAVNSHIGGKGPAPMTQAQPEATN 383
QY 48 D 48
Db 384 D 384
RESULT 21
Q6PDL7_MOUSE
ID Q6PDL7_MOUSE PRELIMINARY; PRT; 874 AA.
AC Q6PDL7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ddx26 protein.
GN Name=Ddx26;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;

AC Q9Z2C8; Q5NCW8; Q5NCW9; Q9Z2C7;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Y-box binding protein 2 (Germ cell specific Y-box binding protein)
DE (FRGY2 homolog).
GN Name=Ybx2; Synonyms=Msy2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC STRAIN=CD-1; TISSUE=Testis;
RX MEDLINE=98455458; PubMed=9780336;
RA Gu W., Tekur S., Reinbold R., Eppig J.J., Choi Y.-C., Zheng J.Z.,
RA Murray M.T., Hecht N.B.;
RT "Mammalian male and female germ cells express a germ cell-specific Y-
box protein, MSY2.";
RL Biol. Reprod. 59:1266-1274(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG The mouse genome sequencing consortium;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION IN MRNA TRANSLATION, PHOSPHORYLATION, RNA-BINDING, AND
RP IDENTIFICATION IN A MRNP COMPLEX WITH PABPC1.
RX PubMed=10076007; DOI=10.1093/nar/27.7.1747;
RA Herbert T.P., Hecht N.B.;
RT "The mouse Y-box protein, MSY2, is associated with a kinase on non-
polyosomal mouse testicular mRNAs.";
RL Nucleic Acids Res. 27:1747-1753(1999).
RN [4]
RP IDENTIFICATION IN A MRNP COMPLEX WITH CSDA.
RC TISSUE=Testis;
RX PubMed=10772793; DOI=10.1006/dbio.2000.9658;
RA Davies H.G., Giorgini F., Fajardo M.A., Braun R.E.;
RT "A sequence-specific RNA binding complex expressed in murine germ
cells contains MSY2 and MSY4.";
RL Dev. Biol. 221:87-100(2000).
RN [5]
RP PHOSPHORYLATION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=11566752;
RA Yu J., Hecht N.B., Schultz R.M.;
RT "Expression of MSY2 in mouse oocytes and preimplantation embryos.";
RL Biol. Reprod. 65:1260-1270(2001).
RN [6]
RP RNA-BINDING.
RX PubMed=11564883; DOI=10.1128/MCB.21.20.7010-7019.2001;
RA Giorgini F., Davies H.G., Braun R.E.;
RT "MSY2 and MSY4 bind a conserved sequence in the 3' untranslated region
of protamine 1 mRNA in vitro and in vivo.";
RL Mol. Cell. Biol. 21:7010-7019(2001).
RN [7]
RP FUNCTION IN MRNA TRANSLATION, AND RNA-BINDING.
RX PubMed=12297523;
RA Yu J., Hecht N.B., Schultz R.M.;
RT "RNA-binding properties and translation repression in vitro by germ
cell-specific MSY2 protein.";
RL Biol. Reprod. 67:1093-1098(2002).
RN [8]
RP FUNCTION IN MATERNAL MRNA CYTOPLASMIC RETENTION, RNA-BINDING, AND
RP MUTAGENESIS OF TYR-109 AND PHE-111.
RX PubMed=12648488; DOI=10.1016/S0012-1606(02)00094-5;
RA Yu J., Hecht N.B., Schultz R.M.;
RT "Requirement for RNA-binding activity of MSY2 for cytoplasmic
localization and retention in mouse oocytes.";
RL Dev. Biol. 255:249-262(2003).
RN [9]
RP FUNCTION IN MRNA STABILITY.
RX PubMed=15031116; DOI=10.1016/j.ydbio.2003.12.020;
RA Yu J., Deng M., Medvedev S., Yang J., Hecht N.B., Schultz R.M.;

RT "Transgenic RNAi-mediated reduction of MSY2 in mouse oocytes results
in reduced fertility.";
RL Dev. Biol. 268:195-206(2004).
RN [10]
RP FUNCTION IN CYTOPLASMIC MRNA STORAGE, RNA-BINDING, AND DNA-BINDING.
RX PubMed=15665108; DOI=10.1073/pnas.0404685102;
RA Yang J., Medvedev S., Reddi P.P., Schultz R.M., Hecht N.B.;
RT "The DNA/RNA-binding protein MSY2 marks specific transcripts for
cytoplasmic storage in mouse male germ cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:1513-1518(2005).
CC -!- FUNCTION: Major constituent of messenger ribonucleoprotein
particles (mRNPs). Involved in the regulation of the stability
and/or translation of germ cell mRNAs. Binds to Y-box consensus
promoter element. Binds to full length mRNA with high affinity in
a sequence-independent manner. Binds to short RNA sequences
containing the consensus site 5'-UCCAUCA-3' with low affinity and
limited sequence specificity. Its binding with maternal mRNAs is
necessary for its cytoplasmic retention. May mark specific mRNAs
(those transcribed from Y-box promoters) in the nucleus for
cytoplasmic storage, thereby linking transcription and mRNA
storage/translational delay.
CC -!- SUBUNIT: Found in a mRNP complex with PABPC1 and CSDA.
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Msy2;
CC IsoId=Q9Z2C8-1; Sequence=Displayed;
CC Name=2; Synonyms=Msy2a;
CC IsoId=Q9Z2C8-2; Sequence=VSP_013052, VSP_013053;
CC Note=In Ref.4 isoform 2 not detected in oocytes;
CC -!- TISSUE SPECIFICITY: Expressed in meiotic and postmeiotic male germ
cells and oocytes; poorly expressed in two cell stage embryos (at
protein level). Not detected in preimplantation embryos.
CC -!- PTM: Phosphorylated during oocyte maturation and dephosphorylated
following egg activation. Phosphorylated in vitro by a kinase
activity associated with testicular mRNPs. Dephosphorylation leads
to a decrease in its affinity to bind RNA in vitro.
CC -!- MISCELLANEOUS: Knockout mice for this gene exhibited reduced level
of mRNA and protein synthesis in fully grown oocytes and decrease
fertility.
CC -!- SIMILARITY: Contains 1 CSD (cold-shock) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; AF073954; AAC98673.1; -; mRNA.
DR EMBL; AF073955; AAC98674.1; -; mRNA.
DR EMBL; AL596185; CAI35155.1; -; Genomic_DNA.
DR EMBL; AL596185; CAI35156.1; -; Genomic_DNA.
DR HSSP; P41016; 1HZA.
DR SMR; Q9Z2C8; 89-166.
DR Ensembl; ENSMUSG0000018554; Mus musculus.
DR MGI; MGI:1096372; Ybx2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0003729; F:mRNA binding; IDA.
DR GO; GO:0045182; F:translation regulator activity; IDA.
DR InterPro; IPR011129; CSP.
DR InterPro; IPR02059; CSP_DNA_bd.
DR InterPro; IPR012340; OB_NA_bd_sub.
DR Pfam; PF00313; CSD; 1.
DR PRINTS; PR00050; COLDSHOCK.
DR ProDom; PD000621; Cold_shock; 1.
DR SMART; SM00357; CSP; 1.
DR PROSITE; PS00352; COLD_SHOCK; 1.
KW Alternative splicing; DNA-binding; Nuclear protein; Phosphorylation;
KW RNA-binding.
FT DOMAIN 95 165 CSD.
FT REGION 89 171 Required for cytoplasmic retention.
FT REGION 219 360 Required for mRNA-binding.
FT COMPIAS 41 57 Gly-rich.

ID	Q5Z9G0_ORYSA	PRELIMINARY;	PRT;	208	AA.
AC	Q5Z9G0;				
DT	25-OCT-2004	(TrEMBLrel. 28, Created)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Hypothetical protein P0655A07.32.				
GN	Name=P0655A07.32;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Ehrhartoidae; Oryzeae; Oryza.				
OX	NCBI_TaxID=39947;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC				
RT	clone:P0655A07.";				
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.				
DR	EMBL; AP003634; BAD53647.1; -; Genomic_DNA.				
KW	Hypothetical protein.				
SQ	SEQUENCE	208	AA;	20992	MW; 455913B4183221D7 CRC64;
Query Match 23.3%; Score 62.5; DB 2; Length 208;					
Best Local Similarity 45.0%; Pred. No. 34;					
Matches 18; Conservative 1; Mismatches 16; Indels 5; Gaps 2;					
QY	5	PRPGAPCRA-GAPTIVLTSGRRQTLSHGSSSPARATLGKP	43		
Db	58	PPQAPCGRRLPPTIL----RSAPSSSMPPPRATLDLP	93		
RESULT 31					
Q8XQ41	RALSO				
ID	Q8XQ41_RALSO	PRELIMINARY;	PRT;	556	AA.
AC	Q8XQ41;				
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	PROBABLE ACTIVATION/SECRETION SIGNAL PEPTIDE PROTEIN.				
GN	OrderedLocusNames=RSpl445; ORFNames=RS03098;				
OS	Ralstonia solanacearum (Pseudomonas solanacearum).				
OG	Plasmid megaplasmid.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;				
OC	Burkholderiaceae; Ralstonia.				
OX	NCBI_TaxID=305;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=GMI1000;				
RX	MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;				
RA	Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,				
RA	Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,				
RA	Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,				
RA	Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,				
RA	Siguiet P., Thebault P., Whalen M., Wincker P., Levy M.,				
RA	Weissenbach J., Boucher C.A.;				
RT	"Genome sequence of the plant pathogen Ralstonia solanacearum.";				
RL	Nature 415:497-502(2002).				
DR	EMBL; AL646084; CAD18596.1; -; Genomic_DNA.				
KW	Complete proteome; Plasmid.				
SQ	SEQUENCE	556	AA;	58835	MW; 5C27CF4AAED0EC72 CRC64;
Query Match 23.3%; Score 62.5; DB 2; Length 556;					
Best Local Similarity 37.5%; Pred. No. 1e+02;					
Matches 18; Conservative 7; Mismatches 22; Indels 1; Gaps 1;					
QY	1	MAAGPRPG-APCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVLN	47		
Db	202	LAAGARPGQTVELVIGSRAAPLTSGRLADNYGSLYTGRTRVGGLNVN	249		
RESULT 32					
Q9Z5X4	FRASE				
ID	Q9Z5X4_FRASE	PRELIMINARY;	PRT;	671	AA.

AC	Q9Z5X4;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Ferredoxin oxidoreductase a-subunit.				
OS	Frankia sp. (strain EuIK1)				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Frankineae; Frankiaceae; Frankia.				
OX	NCBI_TaxID=47227;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=EuIK1;				
RA	Chung-Sun A., Ji-Tae K., Won-Jin K., Won-Young Y.;				
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.				
DR	EMBL; AF119361; AAD17273.1; -; Genomic DNA.				
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.				
DR	GO; GO:0006118; P:electron transport; IEA.				
DR	InterPro; IPR002880; POR_N.				
DR	Pfam; PF01855; POR_N; 1.				
SQ	SEQUENCE	671	AA;	71283	MW; 3EAF14BBBBB36C598 CRC64;
Query Match 23.3%; Score 62.5; DB 2; Length 671;					
Best Local Similarity 38.3%; Pred. No. 1.3e+02;					
Matches 18; Conservative 5; Mismatches 17; Indels 7; Gaps 2;					
QY	1	MAAGPRPGAPCRAGAPTIVLTS-----GRRQTLSHGSSSPARATLGK	42		
Db	540	LPARPRPGAGHRPGAPALPQPAAGEPRGRAVVLRHGAG--AEMNLGQ	584		
RESULT 33					
Q5ZKM6	CHICK				
ID	Q5ZKM6_CHICK	PRELIMINARY;	PRT;	771	AA.
AC	Q5ZKM6;				
DT	25-OCT-2004	(TrEMBLrel. 28, Created)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)			
DE	Hypothetical protein.				
GN	ORFNames=RCJMB04_10a9;				
OS	Gallus gallus (Chicken).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=CB; TISSUE=Bursa;				
RA	Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,				
RA	Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,				
RA	Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;				
RT	"Full-length cDNAs from chicken bursal lymphocytes to facilitate				
RT	genefunction analysis.";				
RL	Genome Biol. 6:R6-R6(2005).				
DR	EMBL; AJ720058; CAG31717.1; -; mRNA.				
KW	Hypothetical protein.				
SQ	SEQUENCE	771	AA;	88312	MW; B26F88692352887F CRC64;
Query Match 23.3%; Score 62.5; DB 2; Length 771;					
Best Local Similarity 42.5%; Pred. No. 1.5e+02;					
Matches 17; Conservative 1; Mismatches 17; Indels 5; Gaps 1;					
QY	2	AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLG	41		
Db	3	AVGPGPGGRRRRRGAPTNIQAQ-----LRHGQLSGRLTRG	37		
RESULT 34					
O93392	COTCO				
ID	O93392_COTCO	PRELIMINARY;	PRT;	215	AA.
AC	O93392;				
DT	01-NOV-1998	(TrEMBLrel. 08, Created)			
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			

DE Pro-alpha2(I) collagen (Fragment).
OS Coturnix coturnix (Common quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=9091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99119493; PubMed=9918878; DOI=10.1006/viro.1998.9499;
RA Oberst C., Hartl M., Weiskirchen R., Bister K.;
RT "Conditional cell transformation by doxycycline-controlled expression
of the MC29 v-myc allele."
RL Virology 253:193-193(1999).
DR EMBL; AF077329; AAD12181.1; -; mRNA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 3.
DR ProDom; PD000007; Clg_helix; 3.
KW Collagen.
FT NON TER 1
SQ SEQUENCE 215 AA; 20194 MW; CDE607AE07D03126 CRC64;

Query Match 23.1%; Score 62; DB 2; Length 215;
Best Local Similarity 37.5%; Pred. No. 41;
Matches 21; Conservative 4; Mismatches 17; Indels 14; Gaps 3;

QY 3 AGPR-----PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVNDYS 50
Db 158 AGPRGPPGSGPPGKGRNGLPGIPGAGVRG--SHGSGQPA---GPPVPLTWS 207
[1]
RESULT 35
Q6ZM28 HUMAN
ID Q6ZM28 HUMAN PRELIMINARY; PRT; 259 AA.
AC Q6ZM28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ1655.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131430; BAD18577.1; -; mRNA.
DR HSSP; P15822; 1BBO.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 2.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.

SQ SEQUENCE 259 AA; 29243 MW; 8CB026415B7559C4 CRC64;

Query Match 23.1%; Score 62; DB 2; Length 259;
Best Local Similarity 30.4%; Pred. No. 50;
Matches 21; Conservative 5; Mismatches 19; Indels 24; Gaps 3;
QY 5 PRPGAPCRAGAPTIVLTSGRR-----QTL-----SHGSSSPARATL----- 40
Db 135 PAPKEPAGPGAPLLVVGSSRNLLSPLSVMSASQALQTVALSAAHGSSEPNLAKALAFN 194
[1]
QY 41 GKPLVLNDY 49
Db 195 GSPLRFDKY 203
[1]

RESULT 36
Q6A047 MOUSE
ID Q6A047 MOUSE PRELIMINARY; PRT; 415 AA.
AC Q6A047;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA0561 protein (Fragment).
GN Name=Mast3; Synonyms=mKIAA0561;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Adult thymus;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries."
RL DNA Res. 11:205-218(2004).
CC -1- SIMILARITY: Contains 1 PDZ·(DHR) domain.
DR EMBL; AK172971; BAD32249.1; -; mRNA.
DR MGI; MGI:2683541; Mast3.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS50106; PDZ; 1.
FT NON TER 1
SQ SEQUENCE 415 AA; 43869 MW; FF7A39DB8ACFA96D0 CRC64;

Query Match 23.1%; Score 62; DB 2; Length 415;
Best Local Similarity 37.8%; Pred. No. 86;
Matches 14; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLG 41
Db 226 PSPTTPCRSPADAPTDTASPPNVSPSSSPASPATG 262
[1]

RESULT 37
Q7SG58 NEUCR
ID Q7SG58 NEUCR PRELIMINARY; PRT; 449 AA.
AC Q7SG58;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU07482.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]

DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNE05190;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15653466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeller K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Perteau M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324 (2005).
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
DR EMBL; AB017345; AAW43739.1; -; Genomic_DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; RVT_1; 1.
DR PROSITE; PS50878; RT_POL; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1059 AA; 116488 MW; 79F19996630E066B CRC64;

Query Match 23.1%; Score 62; DB 2; Length 1059;
Best Local Similarity 29.7%; Pred. No. 2.5e+02;
Matches 19; Conservative 8; Mismatches 15; Indels 22; Gaps 3;

QY 1 MAAGPRPGAPCRAG-----APTIVLTSGRRQTLSHGSSSPARA---TLGKP 43
Db : ||| ||| ||| ||| ||| ||| ||| : : : ||| |||
49 LVACPRCGTGPCSAGTGLSRHQSRVCGLTAPRI-----RRNRVGNSTNTPRRPPSNTAASP 103

QY 44 LVLN 47
Db : || :
104 IVLS 107

RESULT 41
Q55S85_CRYNE PRELIMINARY; PRT; 1059 AA.
AC Q55S85;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNE2970;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;

RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
DR EMBL; AA001000025; EAL20632.1; -; Genomic_DNA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; RVT_1; 1.
DR PROSITE; PS50878; RT_POL; 1.
KW Hypothetical protein.
SQ SEQUENCE 1059 AA; 116568 MW; B52AE531A2E90F1B CRC64;

Query Match 23.1%; Score 62; DB 2; Length 1059;
Best Local Similarity 29.7%; Pred. No. 2.5e+02;
Matches 19; Conservative 8; Mismatches 15; Indels 22; Gaps 3;

QY 1 MAAGPRPGAPCRAG-----APTIVLTSGRRQTLSHGSSSPARA---TLGKP 43
Db : ||| ||| ||| ||| ||| ||| ||| : : : ||| |||
49 LVACPRCGTGPCSAGTGLSRHQSRVCGLTAPRI-----RRNRVGNSTNTPRRPPSNTAASP 103

QY 44 LVLN 47
Db : || :
104 IVLS 107

RESULT 42
RIMB2_CHICK
ID RIMB2_CHICK STANDARD; PRT; 1325 AA.
AC Q8QFX1;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE RIM binding protein 2 (RIM-BP2).
GN Name=RIMBP2; Synonyms=RBP2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, INTERACTIONS WITH RIMS1; RIMS2; CACNA1D AND CACNA1B, AND
RP FUNCTION OF SH3 DOMAIN.
RX MEDLINE=21984561; PubMed=11988172; DOI=10.1016/S0896-6273(02)00667-0;
RA Hibino H., Pironkova R., Onwumere O., Vologodskaya M., Hudspeth A.J.,
RA Lesage F.;
RT "RIM binding proteins (RBPs) couple Rab3-interacting molecules (RIMs)
RT to voltage-gated Ca(2+) channels.";
RL Neuron 34:411-423 (2002).
CC -!- FUNCTION: Plays a role in the synaptic transmission as
CC bifunctional linker that interacts simultaneously with RIMS1,
CC RIMS2, CACNA1D and CACNA1B.
CC -!- SUBUNIT: Interacts with RIMS1, RIMS2, CACNA1D and CACNA1B, and
CC potentially with other Ca(2+) channel alpha-1 isoforms.
CC -!- SUBCELLULAR LOCATION: Synaptic plasma membrane.
CC -!- TISSUE SPECIFICITY: Brain, cochlea and retina.
CC -!- DOMAIN: The SH3 domains mediate binding to a proline-rich motif in
CC RIMS1, RIMS2, CACNA1D and CACNA1B.
CC -!- SIMILARITY: Contains 3 fibronectin type-III domains.
CC -!- SIMILARITY: Contains 3 SH3 domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC

DR EMBL; AY072908; AAL67995.1; -; mRNA.
DR HSSP; P29354; IAZE.
DR SMR; Q8QFX1; 181-261.
DR Ensembl; ENSGALG0000002579; Gallus gallus.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR011511; SH3_2.
DR Pfam; PF00041; fn3; 3.
DR Pfam; PF07653; SH3_2; 3.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 3.
DR SMART; SM00060; FN3; 3.
DR SMART; SM00326; SH3; 3.
DR PROSITE; PS50853; FN3; 3.
DR PROSITE; PS50002; SH3; 3.
KW Membrane; Repeat; SH3 domain.
FT DOMAIN 186 253 SH3 1.
FT DOMAIN 315 395 Fibronectin type-III 1.
FT DOMAIN 409 481 Fibronectin type-III 2.
FT DOMAIN 505 591 Fibronectin type-III 3.
FT DOMAIN 1121 1189 SH3 2.
FT DOMAIN 1225 1292 SH3 3.
SQ SEQUENCE 1325 AA; 147538 MW; 1DD8C50D4CDA1B5B CRC64;

Query Match 23.1%; Score 62; DB 1; Length 1325;
Best Local Similarity 34.5%; Pred. No. 3.2e+02;
Matches 20; Conservative 7; Mismatches 13; Indels 18; Gaps 3;

QY 2 AAGPRP-----GAPCRGAPTIVLTSGRRQTLTSHGSSSPARATLGKPLVL 46
Db 1040 AAGPLAKSHRDAEDSLLLGNPSSAGRPVEHAGRRS--SHGSVPQRS---RPLVL 1092

RESULT 43
Q4SE53 TETNG
ID Q4SE53_TETNG PRELIMINARY; PRT; 1553 AA.
AC Q4SE53;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF14625, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00019708001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAAE01014625; CAG01079.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 1553 AA; 166611 MW; 47624318FEA7B01C CRC64;

Query Match 23.1%; Score 62; DB 2; Length 1553;
Best Local Similarity 35.7%; Pred. No. 3.8e+02;
Matches 20; Conservative 6; Mismatches 24; Indels 6; Gaps 3;

QY 3 AGPRPGAPCRAG-AP-TIVLTSGRRQTLSHG---SSSPARATLGKPLVLNDYSLN 52
Db 476 SGPEPGRCSTGSAPGEVSRGSGEATRPDGGGVSSSPASSTQAGPAALPEVQVD 531

RESULT 44
Q9N2G7 RABIT
ID Q9N2G7_RABIT PRELIMINARY; PRT; 588 AA.
AC Q9N2G7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eukaryotic polypeptide chain release factor 3 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Euthera; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Karamysheva Z.N., Karamyshev A.L., Ito K., Yokogawa T., Nishikawa K.,
RA Nakamura Y., Matsufuji S.;
RT "Antizyme frameshifting as a functional probe of eukaryotic
RT translational termination.";
RL Nucleic Acids Res. 31:5949-5956(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Karamysheva Z., Matsufuji S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035256; BAA92160.1; -; mRNA.
DR HSSP; P02990; 1EFU.
DR GO; GO:0005622; C:intracellular; ISS.
DR GO; GO:0003924; F:GTPase activity; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0003747; F:translation release factor activity; ISS.
DR GO; GO:0000082; P:G1/S transition of mitotic cell cycle; ISS.
DR GO; GO:0000184; P:mRNA catabolism, nonsense-mediated decay; ISS.
DR InterPro; IPR009818; Ataxin-2_C.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR004161; EFTU_D2.
DR InterPro; IPR00795; ProtSyn_GTPbind.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR Pfam; PF07145; PAM2; 1.
DR PRINTS; PR00315; ELONGATNFCT.
DR PROSITE; PS00301; EFACITOR_GTP; UNKNOWN_1.
KW GTP-binding; Nucleotide-binding; Protein biosynthesis.
FT NON TER 1
SQ SEQUENCE 588 AA; 64476 MW; 082A3BCA5757774E CRC64;

Query Match 22.9%; Score 61.5; DB 2; Length 588;
Best Local Similarity 40.4%; Pred. No. 1.5e+02;
Matches 19; Conservative 5; Mismatches 22; Indels 1; Gaps 1;

QY 2 AAGPRPGAPCRGAPTI-VLTSGRRQTLTSHGSSSPARATLGKPLVLN 47
Db 53 AAGNNHAGSVAGGPSAPVSSQEESQSLCEGSISAVSMELSEPVVEN 99

RESULT 45
Q69ZH8 MOUSE
ID Q69ZH8_MOUSE PRELIMINARY; PRT; 1178 AA.
AC Q69ZH8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA1509 protein (Fragment).
GN Name=0610010D24Rik; Synonymus=mkIAA1509;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK173188; BAD32466.1; -;-
DR MGI; MGI:1915589; 0610010D24Rik.
FT NON_TER 1 1
SQ SEQUENCE 1178 AA; 130942 MW; 0E44EF5C79F675BA CRC64;

Query Match 22.9%; Score 61.5; DB 2; Length 1178;
Best Local Similarity 27.8%; Pred. No. 3.2e+02;
Matches 20; Conservative 9; Mismatches 18; Indels 25; Gaps 3;

QY 2 AAGP---RPGAPCRAGAPTIVLTSGRRQTLSHG-----SSSPARAT 39
Db 976 ASGPEACRPESQKPGGHE---AAGARETSTHSLQGSFILARETPIVGKADSPSPGQGT 1032
QY 40 LGKPLVLNDYSL 51
Db 1033 RGRPLDTRRFSL 1044

Search completed: December 27, 2005, 23:04:18
Job time : 230 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2005, 22:57:02 ; Search time 46 Seconds
(without alignments)
93.459 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGAPCRAGAPTIVL.....SSPARATLGKPLVLNDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268	100.0	52	2	US-09-042-225-2
2	74	27.6	16	2	US-09-042-225-8
3	72.5	27.1	173	2	US-09-252-991A-25321
4	67.5	25.2	137	2	US-09-252-991A-30540
5	66	24.6	228	2	US-09-252-991A-28381
6	65	24.3	166	2	US-09-252-991A-16776
7	65	24.3	205	2	US-09-252-991A-31167
8	65	24.3	345	2	US-09-252-991A-25768
9	64.5	24.1	146	2	US-09-252-991A-30866
10	64.5	24.1	149	2	US-09-252-991A-30866
11	63.5	23.7	721	2	US-09-252-991A-28293
12	63	23.5	128	2	US-10-104-047-3112
13	63	23.5	613	2	US-09-252-991A-19955
14	63	23.5	1129	2	US-09-252-991A-22330
15	62	23.1	256	2	US-09-252-991A-25404
16	62	23.1	328	2	US-09-252-991A-19582
17	62	23.1	863	2	US-09-252-991A-26099
18	61.5	22.9	146	2	US-09-949-016-8300
19	61.5	22.9	367	2	US-09-252-991A-19910
20	61.5	22.9	574	2	US-09-252-991A-30868
21	61	22.8	170	2	US-09-252-991A-20706
22	61	22.8	208	2	US-09-252-991A-17849
23	61	22.8	679	2	US-09-252-991A-27111
24	60.5	22.6	155	2	US-09-252-991A-32893
25	60.5	22.6	240	2	US-09-252-991A-28112
26	60	22.4	343	2	US-09-252-991A-27631
27	60	22.4	755	2	US-09-902-540-11169

28	59.5	22.2	158	2	US-09-252-991A-24896	Sequence 24896, A
29	59.5	22.2	293	2	US-09-252-991A-32060	Sequence 32060, A
30	59.5	22.2	395	2	US-09-270-767-44351	Sequence 44351, A
31	59.5	22.2	413	2	US-09-604-231-32	Sequence 32, Appli
32	59.5	22.2	536	2	US-09-359-167-8	Sequence 8, Appli
33	59.5	22.2	606	2	US-09-486-382B-11	Sequence 11, Appli
34	59.5	22.2	683	2	US-09-604-231-30	Sequence 30, Appli
35	59.5	22.2	1031	2	US-09-252-991A-18365	Sequence 18365, A
36	59	22.0	162	2	US-09-252-991A-32101	Sequence 32101, A
37	59	22.0	439	2	US-09-252-991A-17127	Sequence 17127, A
38	59	22.0	770	2	US-09-784-316-5	Sequence 5, Appli
39	59	22.0	770	2	US-10-229-124-5	Sequence 5, Appli
40	58.5	21.8	141	2	US-09-252-991A-23685	Sequence 23685, A
41	58.5	21.8	377	2	US-09-252-991A-32966	Sequence 32966, A
42	58.5	21.8	515	2	US-09-252-991A-23632	Sequence 23632, A
43	58.5	21.8	802	2	US-09-252-991A-25050	Sequence 25050, A
44	58.5	21.8	929	2	US-09-252-991A-19203	Sequence 19203, A
45	58	21.6	117	2	US-09-489-847-199	Sequence 199, App

ALIGNMENTS

RESULT 1
US-09-042-225-2
; Sequence 2, Application US/09042225A
; Patent No. 6207812
; GENERAL INFORMATION:
; APPLICANT: Terek, Richard M.
; TITLE OF INVENTION: CHONDROSARCOMA ASSOCIATED GENES
; FILE REFERENCE: 04930/021001
; CURRENT APPLICATION NUMBER: US/09/042,225A
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-042-225-2

Query Match 100.0%; Score 268; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.9e-27;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAGPRPGAPCRAGAPTIVLTSGRRQTLTSHGSSSPARATLGKPLVLNDYSLN 52
Db 1 MAAGPRPGAPCRAGAPTIVLTSGRRQTLTSHGSSSPARATLGKPLVLNDYSLN 52

RESULT 2
US-09-042-225-8
; Sequence 8, Application US/09042225A
; Patent No. 6207812
; GENERAL INFORMATION:
; APPLICANT: Terek, Richard M.
; TITLE OF INVENTION: CHONDROSARCOMA ASSOCIATED GENES
; FILE REFERENCE: 04930/021001
; CURRENT APPLICATION NUMBER: US/09/042,225A
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-042-225-8

Query Match 27.6%; Score 74; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 RRQTLTSHGSSSPARA 38

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Db          |||||||
1 RRQTLSHGSSSPARA 15

RESULT 3
US-09-252-991A-25321
; Sequence 25321, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25321
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25321

Query Match      27.1%; Score 72.5; DB 2; Length 173;
Best Local Similarity 40.5%; Pred. No. 0.17;
Matches 17; Conservative 4; Mismatches 18; Indels 3; Gaps 1;

Qy 5 PRPGAPCRAGAPTIVLTSGRRQTLSHG---SSSPARATLGKP 43
||| ||||| | : ||: | : | | | | |
Db 44 PRPARACRAGAGTATGAARRRFAGAGPRRAGTPTRAPAGSP 85

RESULT 4
US-09-252-991A-30540
; Sequence 30540, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30540
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30540

Query Match      25.2%; Score 67.5; DB 2; Length 137;
Best Local Similarity 36.0%; Pred. No. 0.54;
Matches 18; Conservative 5; Mismatches 12; Indels 15; Gaps 2;

Qy 2 AAGPRPG-----APCRAGAPTIVLTSGRRQTLSHGSSSPAR 37
| ||||| | ||||| : ||| : | : | | | | |
Db 44 APAPRGRGRGPSIDRRGSPGPRPCLAG-PSAASPCGPRRSIAGGSRSPAR 92

RESULT 5
US-09-252-991A-28381
; Sequence 28381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

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; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28381
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28381

Query Match      24.6%; Score 66; DB 2; Length 228;
Best Local Similarity 38.1%; Pred. No. 1.5;
Matches 16; Conservative 3; Mismatches 9; Indels 14; Gaps 2;

Qy 3 AGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATL-GKP 43
|| || ||||| : | ||| | | | | |
Db 77 AGKAPGAPCRSASP-----HGRSCPPGRLRGRP 105

RESULT 6
US-09-252-991A-16776
; Sequence 16776, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16776
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16776

Query Match      24.3%; Score 65; DB 2; Length 166;
Best Local Similarity 46.2%; Pred. No. 1.4;
Matches 18; Conservative 4; Mismatches 5; Indels 12; Gaps 2;

Qy 4 GPRPGAPCRAGAPTIVLTSGRRQTL-----SHGSSSPARA 38
||||| : | : ||| : | || |||||
Db 115 GPRGSPDR-----SAGRRGSSPPPGSGGSPSPARA 145

RESULT 7
US-09-252-991A-31167
; Sequence 31167, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31167
; LENGTH: 205
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31167

Query Match      24.3%; Score 65; DB 2; Length 205;
Best Local Similarity 32.1%; Pred. No. 1.8;
Matches 18; Conservative 6; Mismatches 18; Indels 14; Gaps 2;

Qy      2 AAGPRPGAPCRAGAPTIV-----LTSGRQTLSHGSSSP-----ARATLGKP 43
Db      142 APGGPARPVRRGGPPAVRRGECFPVRRRAGRRDRASGSAAPPGGDRAAGRGP 197

RESULT 8
US-09-252-991A-25768
; Sequence 25768, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25768
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25768

Query Match      24.3%; Score 65; DB 2; Length 345;
Best Local Similarity 40.5%; Pred. No. 3.4;
Matches 15; Conservative 5; Mismatches 13; Indels 4; Gaps 1;

Qy      5 PRPGAPCRAGAPTIVLTSGRQTLSHGSSSPARATLG 41
Db      150 PTPGAPTRIG---LFCRRRRMSTHWRISPSRPTMG 182

RESULT 9
US-09-252-991A-25930
; Sequence 25930, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25930
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25930

Query Match      24.1%; Score 64.5; DB 2; Length 146;
Best Local Similarity 35.4%; Pred. No. 1.4;
Matches 17; Conservative 5; Mismatches 19; Indels 7; Gaps 1;

Qy      3 AGPRPGAPCRAGAPTIVLTSGRQTLSHGS-----SSPARATLGKP 43
Db      8 ASRSGSPMTAGRWISIPMGSGTRSTATSSPPAGYSRSPSTAVASP 55
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RESULT 10
US-09-252-991A-30866
; Sequence 30866, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30866
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30866

Query Match      24.1%; Score 64.5; DB 2; Length 149;
Best Local Similarity 41.7%; Pred. No. 1.4;
Matches 15; Conservative 2; Mismatches 10; Indels 9; Gaps 1;

Qy      4 GPRPGAPCRAGAPTIVLTSGRQTLSHGSSSPARAT 39
Db      99 GARPGGSCR-----NGRRQSGHAWGSPQRAS 125
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RESULT 11
US-09-252-991A-28293
; Sequence 28293, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28293
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28293

Query Match      23.7%; Score 63.5; DB 2; Length 721;
Best Local Similarity 36.8%; Pred. No. 13;
Matches 21; Conservative 4; Mismatches 17; Indels 15; Gaps 2;

Qy      4 GPRP-----GAPCRAGAPTIVLTSGRQTLSHG-----SSSPARATLGKPLV 45
Db      242 GRRPDPRQAGAPCTARATTGRAGSGRRLLTSRPGCRRWRTCGRPANAAACRRSLGSPSV 298
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RESULT 12
US-10-104-047-3112
; Sequence 3112, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
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; Sequence 26099, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26099
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099
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Query Match 23.1%; Score 62; DB 2; Length 863;
Best Local Similarity 42.4%; Pred. No. 24;
Matches 14; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
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QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPAR 37
|||||
Db 614 PRGPRWRAGAPAGAGCGSRRLRHPAHPQR 646
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RESULT 18
US-09-949-016-8300
; Sequence 8300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8300
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8300
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Query Match 22.9%; Score 61.5; DB 2; Length 146;
Best Local Similarity 41.9%; Pred. No. 3.4;
Matches 18; Conservative 3; Mismatches 21; Indels 1; Gaps 1;
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QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
|||||
Db 103 ATGPSTPPRAAAPSTPATSPGKREDRGLFSIQPAPAGLSLP 145
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```
RESULT 19
US-09-252-991A-19910
; Sequence 19910, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19910
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19910
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Query Match 22.9%; Score 61.5; DB 2; Length 367;
Best Local Similarity 42.5%; Pred. No. 10;
Matches 17; Conservative 5; Mismatches 15; Indels 3; Gaps 2;
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QY 3 AGPRPGAPCRAGA-PTIVLTSGRRQTLSHGSSSPARATLG 41
|||||
Db 311 AAPRPGRPCASRALTPV--PSKPAAYNTGASRPAPASRG 348
|||||
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RESULT 20
US-09-252-991A-30868
; Sequence 30868, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30868
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30868
```

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Query Match 22.9%; Score 61.5; DB 2; Length 574;
Best Local Similarity 43.2%; Pred. No. 17;
Matches 16; Conservative 2; Mismatches 14; Indels 5; Gaps 1;
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```
QY 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLG 41
|||||
Db 388 PRPWRDCPAGAPGAV-----RDSRPAGTGCPRRATPG 419
|||||
```

```
RESULT 21
US-09-252-991A-20706
; Sequence 20706, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20706
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20706
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27631
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27631

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Query Match 22.4%; Score 60; DB 2; Length 343;
Best Local Similarity 41.3%; Pred. No. 14;
Matches 19: Conservative 5: Mismatches 12: Indels 10: Gaps 4;

QY 5 PRPGAPCRAGAP-TIVLTSGRR--QTL----SHGSSSPARATLGKP 43
 ||||| ||| ||| ||| ||| :|||: |||
 Db 169 PHPGRP---GLPREVLGSGHRHLODLADPPTHGASVSAGTSGSP 211

RESULT 27
US-09-902-540-11169
; Sequence 11169, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B

```

; FILE REFERENCE: 30-10(15047) D
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11169
; LENGTH: 755
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11169

```

Query Match	22.4%;	Score 60;	DB 2;	Length 755;
Best Local Similarity	30.4%;	Pred. No. 37;		
Matches 14: Conservative		7: Mismatches	19: Indels	6: Gaps
				1;

Qy
1 MAAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVL 46
:
: | | | | | : : : : :
db
365 LPALPGGAPPEPVGVPPLDAASRTWGM-----PRAVTLGAPIIV 404

RESULT 28
US-09-252-991A-24896
; Sequence 24896, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

```

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

```

```

; SEQ ID NO 24890
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24896

```

Query Match 22.2%; Score 59.5; DB 2; Length 158;

		Best Local Similarity Matches	32.7%; 16;	Pred: No. 6.6; 5;	Mismatches	21;	Indels	7;	Gaps	1;
QY	2	AAGPRPGAPCRAGA	-----	PTIVLTSGRRQTL	SHGSSSPARATL	GKP	43			
		:			:	:	:	:	:	:
DB	28	SAGAMPGPRMAGSRSSGR	PSNATPASSNRRLRQ	NPNSPIRVP	SGTGP	76				
		:			:	:	:	:	:	:

RESULT 29
US-09-252-991A-32060
; Sequence 32060, Application US/09252991A
: Patent No. 6551795

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/ GENERAL INFORMATION.
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142

```

Query Match 22.2%; Score 59.5; DB 2; Length 293;
Best Local Similarity 37.8%; Pred. No. 14;
Matches 17; Conservative 4; Mismatches 19; Indels

Qy

3 AGPRPGACRAGACTIVLTSGRRQTLSHGSSPA-----RATLGKP 43
||||| :|: :| | ||| |

pB

130 AGPRPDGTSAGSOPVLLRAA-RPAPDHGGPPAAQRTORAPAGKP 173
||||| :|: :| | ||| |

RESULT 30
US-09-270-767-44351
; Sequence 44351, Application US-09270767

```

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44351
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44351

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	Query Match	22.2%	Score 59.5;	DB 2;	Length 395;
	Best Local Similarity	34.0%	Pred. No. 20;		
	Matches 18;	Conservative	5;	Mismatches 19;	Indels 11; Gaps 2;
Qy	2	AAGPRPGAPCRAGA-----	PTIVLTSGRRQTL	SHGSSSPARA-----	TLGKP 43
Dh	163	ACGGCAGPIPAKAGATGIP	CPAVAAAAPGAPATOSAVTTT	ATAAAAAPAIAPOTTITKP	215

RESULT 31
US-09-604-231-32
; Sequence 32, Application US/09604231
; Patent No. 6884614
; GENERAL INFORMATION:

RESULT 45
US-09-489-847-199
; Sequence 199, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-199

Query Match 21.6%; Score 58; DB 2; Length 117;
Best Local Similarity 30.4%; Pred. No. 7.2;
Matches 17; Conservative 4; Mismatches 19; Indels 16; Gaps 1;

QY 1 MAAAGPRPGA-----PCRAGAPTIVLTSGRRQTLSHGSSSPARATL 40
:|||||
Db 18 LAAGPTPSTGSSPSWKQHIGTSLQKTRGSLPTTTLTSGAGQSTSTGKNPAAGRSL 73

Search completed: December 27, 2005, 23:05:52
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: December 27, 2005, 23:04:24 ; Search time 163 Seconds
(without alignments)
133.295 Million cell updates/sec

Title: US-09-819-144A-2
 Perfect score: 268
 Sequence: 1 MAAGRRGACPRAGAPTIVL.....SSPARATLGKPLVLDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 s
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	268	100.0	52	3	US-09-819-144A-2	Sequence 2, Appli
2	79	29.5	229	4	US-10-425-115-222906	Sequence 222906,
3	77	28.7	190	4	US-10-437-963-198300	Sequence 198300,
4	74	27.6	16	3	US-09-819-144A-8	Sequence 8, Appli
5	73.5	27.4	791	4	US-10-170-385-57	Sequence 57, Appli
6	73.5	27.4	863	4	US-10-359-012-2	Sequence 2, Appli
7	73.5	27.4	863	4	US-10-359-012-14	Sequence 14, Appli
8	71.5	26.7	240	4	US-10-425-115-226148	Sequence 226148,
9	71	26.5	19608	4	US-10-084-846A-8	Sequence 8, Appli
10	68	25.4	315	4	US-10-080-170-423	Sequence 423, App
11	68	25.4	315	4	US-10-080-170-423	Sequence 423, App
12	68	25.4	315	4	US-10-468-356-423	Sequence 423, App
13	67	25.0	219	4	US-10-425-115-262578	Sequence 262578,
14	67	25.0	1321	5	US-10-840-512-117	Sequence 117, App
15	66.5	24.8	185	4	US-10-425-115-341679	Sequence 341679,
16	65.5	24.4	923	5	US-10-756-149-5246	Sequence 5246, Ap
17	64.5	24.1	137	4	US-10-767-701-33507	Sequence 33507, A
18	64.5	24.1	309	5	US-10-450-763-43334	Sequence 43334, A
19	64.5	24.1	596	4	US-10-156-761-8931	Sequence 8931, Ap
20	64	23.9	165	4	US-10-425-115-270067	Sequence 270067,
21	64	23.9	359	4	US-10-437-963-190864	Sequence 190864,
22	63.5	23.7	74	4	US-10-425-115-263976	Sequence 263976,
23	63.5	23.7	87	4	US-10-425-115-313357	Sequence 313357,
24	63.5	23.7	223	4	US-10-425-114-62626	Sequence 62626, A
25	63	23.5	128	4	US-10-104-047-3112	Sequence 3112, Ap
26	63	23.5	128	4	US-10-108-260A-2594	Sequence 2594, Ap
27	62.5	23.3	118	4	US-10-424-599-271704	Sequence 271704,

28	62.5	23.3	197	4	US-10-437-963-128246	Sequence 128246,
29	62.5	23.3	208	4	US-10-437-963-176133	Sequence 176133,
30	62.5	23.3	524	5	US-10-450-763-38710	Sequence 38710, A
31	62	23.1	79	4	US-10-425-115-259836	Sequence 259836,
32	62	23.1	175	4	US-10-425-115-210919	Sequence 210919,
33	62	23.1	177	4	US-10-437-963-109208	Sequence 109208,
34	62	23.1	259	4	US-10-443-622-59	Sequence 59, Appl
35	62	23.1	259	5	US-10-974-440-30	Sequence 30, Appl
36	61.5	22.9	135	4	US-10-425-115-350149	Sequence 350149,
37	61.5	22.9	154	4	US-10-767-701-55508	Sequence 55508, A
38	61.5	22.9	170	3	US-09-864-408A-6684	Sequence 6684, Ap
39	61.5	22.9	240	4	US-10-425-115-326091	Sequence 326091,
40	61	22.8	79	4	US-10-425-115-357643	Sequence 357643,
41	61	22.8	169	4	US-10-767-701-42973	Sequence 42973, A
42	61	22.8	176	4	US-10-425-115-203617	Sequence 203617,
43	61	22.8	241	4	US-10-425-115-245202	Sequence 245202,
44	61	22.8	595	4	US-10-156-761-10072	Sequence 10072, A
45	61	22.8	656	4	US-10-108-260A-2611	Sequence 2611, Ap

ALIGNMENTS

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RESULT 1
US-09-819-144A-2
; Sequence 2, Application US/09819144A
; Publication No. US20010016649A1
; GENERAL INFORMATION:
; APPLICANT: Terek, Richard M.
; TITLE OF INVENTION: CHONDROSARCOMA ASSOCIATED GENES
; FILE REFERENCE: 21486-021DIV
; CURRENT APPLICATION NUMBER: US/09/819.144A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-144A-2

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Query Match      100.0%; Score 268; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. NO. 2.6e-24;
Matches 52: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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RESULT 2
US-10-425-115-222906
; Sequence 222906, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 222906

```

LOCATION: (1): (425)
OTHER INFORMATION: unsure at all Xaa locations


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US-10-359-012-14
; Sequence 14, Application US/10359012
; Publication No. US20030232419A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: KOLODKIN, Alex L.
; APPLICANT: TERMAN, Jon R.
; APPLICANT: MAO, Tianyi
; APPLICANT: PASTERKAMP, Ronald J.
; APPLICANT: YU, Hung-Hsiang
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/388,325
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/384,302
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/354,178
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-359-012-14

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Query Match	26.5%;	Score 71;	DB 4;	Length 19608;
Best Local Similarity	39.6%;	Pred. No. 4.8e+02;		
Matches 19;	Conservative	2;	Mismatches 15;	Indels 12;
				Gaps 2;

QY	2	AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGS-----SSPARATLGP	43
Db	3641	ARPPRPGRHCRGGAP-----GKRSGRSRGTAALADSSPGRTARSGP	3682

RESULT 10
US-10-080-170-423
; Sequence 423, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 423
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-423

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Query Match      25.4%; Score 68; DB 4; Length 315;
Best Local Similarity 28.2%; Pred. NO. 11;
Matches 20; Conservative 5; Mismatches 14; Indels 32; Gaps 2
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; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8931
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8931

Query Match 24.1%; Score 64.5; DB 4; Length 596;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 18; Conservative 3; Mismatches 10; Indels 5; Gaps 1;

QY 11 CR-----AGAPTIVLTSGRRQTLSHGSSSPARATLG 41
||| ||| | ||| | ||| : ||| : ||
Db 288 CRREDSAGAVRVRLLIGRLQPTSAGSASPARSSLG 323

RESULT 20
US-10-425-115-270067
; Sequence 270067, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 270067
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177899C.1.pep
US-10-425-115-270067

Query Match 23.9%; Score 64; DB 4; Length 165;
Best Local Similarity 38.2%; Pred. No. 16;
Matches 13; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 4 GPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPAR 37
||| ||| | | : || : | : |
Db 83 GPSRPCRRGGPRRSGRPRTPASGTEASRR 116

RESULT 21
US-10-437-963-190864
; Sequence 190864, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 190864
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87238C.1.pep
US-10-437-963-190864

Query Match 23.9%; Score 64; DB 4; Length 359;
Best Local Similarity 30.0%; Pred. No. 38;
Matches 24; Conservative 6; Mismatches 14; Indels 36; Gaps 4;

QY 2 AAGPRPGAPCRAGA-PTIVLTS----GRRQ-----T 27
||| ||| : ||| | ||| : |||
Db 176 AAAPRSGTSRRGARPEIALTNELGKRRERAPHLHPQRPRRGGTYTTTAAATFPVQ 235
;
QY 28 LSHGSSSPARATLGKPLVLN 47
||| | : | | | : |
Db 236 LSHSSPNPIRTPL--PFLLD 253

RESULT 22
US-10-425-115-263976
; Sequence 263976, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263976
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172359C.1.pep
US-10-425-115-263976

Query Match 23.7%; Score 63.5; DB 4; Length 74;
Best Local Similarity 48.6%; Pred. No. 7.6;
Matches 17; Conservative 0; Mismatches 9; Indels 9; Gaps 2;

QY 3 AGPR--PGAPCRAGAPTIVLTSGRRQTLSHGSSSP 35
||| | | | | | | | | | |
Db 2 AGPRAPPGVPRAGA-----GRRAGPRHGPREP 29

RESULT 23
US-10-425-115-313357
; Sequence 313357, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115


```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 313357
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_4883C.1.pep
US-10-425-115-313357

Query Match      23.7%; Score 63.5; DB 4; Length 87;
Best Local Similarity 33.3%; Pred. No. 9.1;
Matches 17; Conservative 4; Mismatches 13; Indels 17; Gaps 3;

QY      5 PRPGAP-----CRAGAPTIVLTSGRRQTLHGSSSPARATLGKP 43
      ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      21 PNEGAPNYSKTPEQTREACKRGPPPL----GRGE-LGDGLGAPGNGVLGKP 66

RESULT 24
US-10-425-114-62626
; Sequence 62626, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62626
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-112-D11_FLI.pep
US-10-425-114-62626

Query Match      23.7%; Score 63.5; DB 4; Length 223;
Best Local Similarity 34.8%; Pred. No. 26;
Matches 16; Conservative 8; Mismatches 21; Indels 1; Gaps 1;

QY      2 AAGPRGAPCR-AGAPTIVLTSGRRQTLHGSSSPARATLGKPLVL 46
      :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      106 SAGPRPSSTRPPWAAAAAARARRRLLPRGAASPRRRPRRPRLL 151

RESULT 25
US-10-104-047-3112
; Sequence 3112, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3112
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3112
```

```

Query Match      23.5%; Score 63; DB 4; Length 128;
Best Local Similarity 35.6%; Pred. No. 16;
Matches 16; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY      4 GPRPGAPCRAGAPTIVLTSGRRQTLHGSSSPARATLGKPLVLND 48
      ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      2 GPAAGHAAPRGPPVPATTAG--AALRAGASEPRQTQLGAPLALGE 44

RESULT 26
US-10-108-260A-2594
; Sequence 2594, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2594
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2594

Query Match      23.5%; Score 63; DB 4; Length 128;
Best Local Similarity 35.6%; Pred. No. 16;
Matches 16; Conservative 4; Mismatches 23; Indels 2; Gaps 1;

QY      4 GPRPGAPCRAGAPTIVLTSGRRQTLHGSSSPARATLGKPLVLND 48
      ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      2 GPAAGHAAPRGPPVPATTAG--AALRAGASEPRQTQLGAPLALGE 44

RESULT 27
US-10-424-599-271704
; Sequence 271704, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 271704
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87368C.1.pep
US-10-424-599-271704

Query Match      23.3%; Score 62.5; DB 4; Length 118;
Best Local Similarity 38.3%; Pred. No. 17;
Matches 18; Conservative 5; Mismatches 19; Indels 5; Gaps 1;

QY      2 AAGPRPGAPCRAGAPTIVLTSGRRQTL-----HGSSSPARATLGKP 43
      ||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      15 APRPPPGAPPPGSGPPPLGSGPRSGACAPPGCGGASAPARASVGAP 61

RESULT 28
US-10-437-963-128246
; Sequence 128246, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128246
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(197)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30618C.1.pep
US-10-437-963-128246

Query Match 23.3%; Score 62.5; DB 4; Length 197;
Best Local Similarity 39.5%; Pred. No. 30;
Matches 17; Conservative 4; Mismatches 17; Indels 5; Gaps 2;

Qy 2 AAGPRPGAPCRGAPTIVLTSGRRQTLSHGSSSPAR--ATLGK 42
Db 3 AAGPSSSAPPRPGAGVATMAAGRR---GHGDGDGAALGAAVGR 42

RESULT 29
US-10-437-963-176133
; Sequence 176133, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176133
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73911C.1.pep
US-10-437-963-176133

Query Match 23.3%; Score 62.5; DB 4; Length 208;
Best Local Similarity 45.0%; Pred. No. 31;
Matches 18; Conservative 1; Mismatches 16; Indels 5; Gaps 2;

Qy 5 PRPGAPCRA-GAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
Db 58 PPPQAPCRGRRLPTIL----RSAPSSSSMPPPRATIDLDP 93

RESULT 30
US-10-450-763-38710

; Sequence 38710, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 38710
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (120)..(458)
; OTHER INFORMATION: AIR synthase related protein domain identified by Pfam,
; OTHER INFORMATION: accession name AIRS, E-value=1.8e-06, Pfam score of -5.1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(524)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-38710

Query Match 23.3%; Score 62.5; DB 5; Length 524;
Best Local Similarity 44.7%; Pred. No. 88;
Matches 17; Conservative 3; Mismatches 11; Indels 7; Gaps 2;

Qy 10 PCRGAPTIVLTS----GRRQTLSHGSSSPARATLGK 42
Db 9 PCRAGA--MAETSATGACGEAMAAAEAGSSGPAGLTLGR 44

RESULT 31
US-10-425-115-259836
; Sequence 259836, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259836
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_168589C.1.pep
US-10-425-115-259836

Query Match 23.1%; Score 62; DB 4; Length 79;
Best Local Similarity 37.8%; Pred. No. 12;
Matches 14; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

Qy 7 PGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
Db 6 PSSPCRVSASVSTAQTRPRLFVS--ARAPARRTCGKP 40

RESULT 32

```
US-10-425-115-210919
; Sequence 210919, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 210919
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_123954C.1.pep
US-10-425-115-210919

Query Match      23.1%; Score 62; DB 4; Length 175;
Best Local Similarity 45.2%; Pred. No. 30;
Matches 14; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY      10 PCRAGAPTIVLTSGRRQTLSHGSSSPARATL 40
Db      78 PTSAAPPSLWSSPGRLOPHAHGSSPPHRAPL 108

RESULT 33
US-10-437-963-109208
; Sequence 109208, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109208
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(177)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13388C.1.pep
US-10-437-963-109208

Query Match      23.1%; Score 62; DB 4; Length 177;
Best Local Similarity 42.9%; Pred. No. 30;
Matches 15; Conservative 2; Mismatches 16; Indels 2; Gaps 1;

QY      5 PRGPACPRAGAPTIVLTSGRRQTLS--HGSSSPAR 37
Db      96 PRPPASARRSPPLAAAGPRATARRIHSRSPAR 130

RESULT 34
US-10-443-622-59
```

```
; Sequence 59, Application US/10443622
; Publication No. US20040024192A1
; GENERAL INFORMATION:
; APPLICANT: Carter et al.
; TITLE OF INVENTION: 19 Human Secreted Proteins
; FILE REFERENCE: P2009P1
; CURRENT APPLICATION NUMBER: US/10/443,622
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT/US98/13608
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 60/051,480
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/051,381
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/058,663
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,598
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (78)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-443-622-59

Query Match      23.1%; Score 62; DB 4; Length 259;
Best Local Similarity 30.4%; Pred. No. 46;
Matches 21; Conservative 5; Mismatches 19; Indels 24; Gaps 3;

QY      5 PRPGAPCRAGAPTIVLTSGRR-----QTL-----SHGSSSPARATL----- 40
Db      135 PAPKEPAGPGAPLLVVGSSRNLLSPLSVMSASQALQTVALSAAHGSSSEPNLALKALAFN 194

QY      41 GKPLVLNDY 49
Db      195 GSPLRFDKY 203

RESULT 35
US-10-974-440-30
; Sequence 30, Application US/10974440
; Publication No. US20050214795A1
; GENERAL INFORMATION:
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BANDMAN, Olga
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: REDDY, Roopa
; APPLICANT: TANG, Y. Tom
; APPLICANT: GERSTIN, Edward H.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Valda
; APPLICANT: LU, Dyung Aina M.
; TITLE OF INVENTION: Human Transcriptional Regulator Molecules
; FILE REFERENCE: PF-0509 USN
; CURRENT APPLICATION NUMBER: US/10/974,440
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US/09/674,743
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/09935
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/084,254
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/095,827
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/102,745
; PRIOR FILING DATE: 1998-10-02
```

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; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 259
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyt
US-10-974-440-30

```

Query Match	23.1%;	Score 62;	DB 5;	Length 259;
Best Local Similarity	30.4%;	Pred. No. 46;		
Matches	21;	Conservative	5;	Mismatches 19;
				Indels 24;
				Gaps 3;

QY	5	PRPGAPCRAGAPTIVLTSGRR	-----QTL-----	SHGSSSPARATL	----	40
Db	135	PAPKEPAGCAPLLVVGSSRNLLSPLSVMSASQALQTVLSAHSSESSEPNLAKALAFN				194
QY	41	GKPLVLNDY	49			
Db	195	GSPLRFDKY	203			

RESULT 36
 US-10-425-115-350149
 ; Sequence 350149, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 350149
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_82508C.1.pep
 US-10-425-115-350149

```

Query Match      22.9%; Score 61.5; DB 4; Length 135;
Best Local Similarity 40.9%; Pred. No. 26;
Matches 18; Conservative 1; Mismatches 22; Indels 3; Gaps 1;

QY    3   AGPRPGAPCRAGAPTIVLTSGRRQT---LSHGSSSPARATLGKP 43
      ||| |||| | : ||| | | | | | | | | | | | | |
Db     1   AWPSPGAPPGGGTTPSSCSAPGRTPCWGGTSARSRPPPERTLTGP 44

```

RESULT 37
US-10-767-701-55508
; Sequence 55508, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55508
; LENGTH: 154
; TYPE: PRT

```

; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30163676.pcp
US-10-767-701-55508

```

Query Match 22.9%; Score 61.5; DB 4; Length 154;
Best Local Similarity 38.5%; Pred. No. 30;
Matches 20; Conservative 4; Mismatches 17; Indels 11; Gaps 3;

Qy	3	AGPRPGAPCRA---GAPTIVLTSGRR-----QTLSHGSSSPARATLGKPLVL 46
Db	65	AAARPSPARSRRDRGGPR---ASGRRMKSRSRTSRHGCAMPMPPTLPLPLPL 113

```

RESULT 38
US-09-864-408A-6684
; Sequence 6684, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1e1
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6684
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (138)..(138)
; OTHER INFORMATION: Wherein Xaa may be any
US-09-864-408A-6684

```

Query Match	22.9%;	Score 61.5;	DB 3;	Length 170;
Best Local Similarity	32.2%;	Pred. No. 33;		
Matches 19;	Conservative	4;	Mismatches 13;	Indels 23;
				Gaps 3;

Qy	6	RPGAP-----CRAG-----	APTVLTSGRR--QTLSHGSSSPARATLG	41
			:	:
			:	:
			:	:
Db	92	RPGIPISLTMTTCRCGRRFPTTPLPPAASPTVSRPSGRNTSPT	TSXDGSSAPLRPAVG	150

```

RESULT 39
US-10-425-115-326091
; Sequence 326091, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecule
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 326091
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(240)
; OTHER INFORMATION: unsure at all Xaa loc
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577 604

```


S-10-767-701-42973

Q: E P B P C A B C P A G A - - - - P T T V I T S G P P O T I S H G S S S P A P A T I G K P 43

Db 76 PRPTPCCSGSRWRPPT-----RRPTPPSPSTSPPRCRSGTP 112

RESULT 44
US-10-156-761-10072
; Sequence 10072, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10072
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10072

Query Match 22.8%; Score 61; DB 4; Length 595;
Best Local Similarity 34.8%; Pred. No. 1.5e+02;
Matches 16; Conservative 3; Mismatches 27; Indels 0; Gaps 0;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKPLVLN 47
Db 487 AANGRPGQRGVFGAPEPTARPGSSATASRGAGTSEAVTGRPSARN 532

RESULT 45
US-10-108-260A-2611
; Sequence 2611, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2611
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2611

Query Match 22.8%; Score 61; DB 4; Length 656;
Best Local Similarity 36.4%; Pred. No. 1.7e+02;
Matches 20; Conservative 6; Mismatches 21; Indels 8; Gaps 3;

QY 2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHG-----SSSPARATLGKPLVNDYS 50
Db 348 ASSPSPAP-RPERPESLLVSGPSVTLTEGLGTVRPEQDPAKSP-GSPLLLRGLS 400

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 23:05:09 ; Search time 12 Seconds
(without alignments)
30.909 Million cell updates/sec

Title: US-09-819-144A-2
Perfect score: 268
Sequence: 1 MAAGPRPGACRAGAPTIVL.....SSPARATLGKPLVINDYSLN 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppe:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppe:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppe:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.ppe:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.ppe:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.ppe:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.ppe:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.ppe:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	57.5	21.5	1614	7	US-11-108-528-82		Sequence 82, Appl
2	57	21.3	575	6	US-10-131-826A-128		Sequence 128, App
3	56	20.9	1306	6	US-10-995-561-1027		Sequence 1027, Ap
4	54.5	20.3	368	7	US-11-000-463-916		Sequence 916, App
5	54.5	20.3	388	7	US-11-000-463-444		Sequence 444, App
6	54	20.1	138	6	US-10-667-295-176		Sequence 176, App
7	54	20.1	2011	7	US-11-080-991-56		Sequence 56, Appl
8	53	19.8	1166	6	US-10-821-234-964		Sequence 964, App
9	53	19.8	1466	7	US-11-186-284-33		Sequence 33, Appl
10	51.5	19.2	184	6	US-10-467-657-2790		Sequence 2790, Ap
11	51.5	19.2	259	6	US-10-512-184-34		Sequence 34, Appl
12	51.5	19.2	269	7	US-11-015-546A-10		Sequence 10, Appl
13	51.5	19.2	371	6	US-10-512-184-71		Sequence 71, Appl
14	51.5	19.2	626	6	US-10-512-184-49		Sequence 49, Appl
15	51.5	19.2	1493	7	US-11-004-057-4		Sequence 4, Appli
16	51.5	19.2	1493	7	US-11-004-057-21		Sequence 21, Appl
17	51.5	19.2	3690	6	US-10-995-561-1016		Sequence 1016, Ap
18	51.5	19.2	3714	6	US-10-995-561-1015		Sequence 1015, Ap
19	51.5	19.2	3717	6	US-10-821-234-1076		Sequence 1076, Ap
20	51	19.0	218	7	US-11-143-980-33		Sequence 33, Appl
21	51	19.0	1618	6	US-10-984-645-2		Sequence 2, Appli
22	50.5	18.8	637	6	US-10-821-234-961		Sequence 961, App
23	50	18.7	529	6	US-10-821-234-1168		Sequence 1168, Ap
24	50	18.7	594	6	US-10-131-826A-10		Sequence 10, Appl
25	50	18.7	2630	7	US-11-186-731-2		Sequence 2, Appli

26	50	18.7	7968	7	US-11-186-731-5	Sequence 5, Appli
27	49.5	18.5	177	6	US-10-999-866-61	Sequence 61, Appl
28	49.5	18.5	205	6	US-10-995-561-1028	Sequence 1028, Ap
29	49.5	18.5	205	6	US-10-995-561-1029	Sequence 1029, Ap
30	49.5	18.5	367	6	US-10-131-826A-208	Sequence 208, App
31	49.5	18.5	441	6	US-10-467-657-3438	Sequence 3438, Ap
32	49.5	18.5	480	7	US-11-132-142-6	Sequence 6, Appli
33	49.5	18.5	1464	7	US-11-000-463-243	Sequence 243, App
34	49.5	18.5	1464	7	US-11-186-284-28	Sequence 28, Appl
35	49.5	18.5	1467	6	US-10-821-234-1096	Sequence 1096, Ap
36	49.5	18.5	1823	6	US-10-995-561-988	Sequence 988, App
37	49.5	18.5	2102	6	US-10-995-561-990	Sequence 990, App
38	49.5	18.5	2108	6	US-10-995-561-989	Sequence 989, App
39	49.5	18.5	2157	6	US-10-995-561-991	Sequence 991, Appl
40	49.5	18.5	3063	7	US-11-186-284-26	Sequence 26, Appl
41	49	18.3	407	6	US-10-995-561-1014	Sequence 1014, Ap
42	49	18.3	707	7	US-11-186-284-132	Sequence 132, App
43	48.5	18.1	188	6	US-10-467-657-920	Sequence 920, App
44	48	17.9	432	6	US-10-467-657-7234	Sequence 7234, Ap
45	48	17.9	599	7	US-11-109-157A-3	Sequence 3, Appli

ALIGNMENTS

```

RESULT 1
US-11-108-528-82
; Sequence 82, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 1614
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-82

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Query Match	21.5%	Score 57.5;	DB 7;	Length 1614;
Best Local Similarity	32.1%;	Pred. No. 16;		
Matches 17; Conservative	7;	Mismatches 18;	Indels 11;	Gaps 2;

Qy 4 GRPGAPC-RAGAPTIVLTSGRRQT-----LSHGSSSPARATLKGKPLV 45
||| ||| : : ||| | ||| : ||| : :
dh 1445 GRPGIPCKSVMSWSLVGGRGSVPLYDRNHVTGASSSSSSSTKATLYPPI 1497

RESULT 2
US-10-131-826A-128
; Sequence 128, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

```
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 128
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-128

Query Match      21.3%; Score 57; DB 6; Length 575;
Best Local Similarity 31.5%; Pred. No. 5.7;
Matches 17; Conservative 7; Mismatches 18; Indels 12; Gaps 2;

QY      1 MAAGPRP-----GAPCRAGPTIVLTSGRRQTLSHGSSSPARATLGKP 43
      : : ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      113 LSTGPAPAMATTSSKPEGRPRGQAAPTILLTKPPGAT-SRPTTAPPRTTTRRP 165

RESULT 3
US-10-995-561-1027
; Sequence 1027, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1027
; LENGTH: 1306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1027
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Query Match      20.9%; Score 56; DB 6; Length 1306;
Best Local Similarity 32.0%; Pred. No. 20;
Matches 16; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

QY      3 AGPRGAPCRAGPTIVLTSGRRQTLSHGSSSPARATLGKPLVLNDYSLN 52
      || ||| | | : : ||| | | : : | | | | : | : | : | : | : | : |
Db      17 AGLGSGAPALSG--SCLLTSGRCRCHRHRTALSIHPPPLARPLFWSQFLH 64

RESULT 4
US-11-000-463-916
; Sequence 916, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 916
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-916

Query Match      20.3%; Score 54.5; DB 7; Length 368;
Best Local Similarity 52.0%; Pred. No. 7;
Matches 13; Conservative 1; Mismatches 8; Indels 3; Gaps 1;

QY      4 GPRPGAPCRAGPTIVLT---SGRR 25
      ||||| | | | | | | | | | | | | | | | |
Db      254 GPRPGMPHPKGAPAFQLNRSLSGQR 278

RESULT 5
US-11-000-463-444
; Sequence 444, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
```



```
; APPLICANT: BURGART, LAWRENCE J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 33
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-33

Query Match      19.8%; Score 53; DB 7; Length 1466;
Best Local Similarity 42.9%; Pred. No. 53;
Matches 18; Conservative 3; Mismatches 17; Indels 4; Gaps 3;

QY      2 AAGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPARATLGKP 43
      ||||| ||| : ||| : ||| ||| : ||| : ||| : |||
Db      709 AAGP-PGPPGAAGTGLQMPGERGGL--GSPGP-KGDKGEP 746

RESULT 10
US-10-467-657-2790
; Sequence 2790, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2790
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2790

Query Match      19.2%; Score 51.5; DB 6; Length 184;
Best Local Similarity 28.9%; Pred. No. 7.5;
Matches 13; Conservative 7; Mismatches 20; Indels 5; Gaps 1;

QY      13 AGAPTIVLTSGRRQTL-----HGSSSPARATLGKPLVLNDYSLN 52
      : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      49 SAADNSIMTKGQKVYESNCIACHGKGEGRGTAFPPLFRSDYIMN 93

RESULT 11
US-10-512-184-34
; Sequence 34, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
```

```
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-34

Query Match      19.2%; Score 51.5; DB 6; Length 259;
Best Local Similarity 39.5%; Pred. No. 11;
Matches 15; Conservative 3; Mismatches 11; Indels 9; Gaps 1;

QY      5 PRPGAPCRAGAPTIVLTSGRRQTLSHGSS 33
      ||| ||| ||| ||| : |||
Db      133 PGPGEGSTKGAPEIVLTQSPSSLAMSVGQKVTMSCKSS 170

RESULT 12
US-11-015-546A-10
; Sequence 10, Application US/11015546A
; Publication No. US20050250126A1
; GENERAL INFORMATION:
; APPLICANT: GAO, ZEREN
; APPLICANT: SHEPPARD, PAUL O.
; APPLICANT: FOX, BRIAN A.
; APPLICANT: HOLLOWAY, JAMES L.
; APPLICANT: JASPERS, STEPHEN R.
; APPLICANT: APPELBY, MARK
; TITLE OF INVENTION: Ztnf13, A TUMOR NECROSIS FACTOR
; FILE REFERENCE: 03-24
; CURRENT APPLICATION NUMBER: US/11/015,546A
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 60/530,185
; PRIOR FILING DATE: 2003-12-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-015-546A-10

Query Match      19.2%; Score 51.5; DB 7; Length 269;
Best Local Similarity 27.7%; Pred. No. 12;
Matches 13; Conservative 6; Mismatches 9; Indels 19; Gaps 2;

QY      1 MAAGPRPGAPCRAGAPTIVLTSGR-----RQTLSHGS 32
      : : ||| ||| : ||| : ||| : ||| : |||
Db      211 LPSAPRPAAPC----PALCLQAERSRRRVFSPWTDSELSSREPLEHGA 253

RESULT 13
US-10-512-184-71
; Sequence 71, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
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RESULT 22
US-10-821-234-961
; Sequence 961, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 961
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-961

Query Match      18.8%; Score 50.5; DB 6; Length 637;
Best Local Similarity 29.2%; Pred. No. 42;
Matches 14; Conservative 7; Mismatches 20; Indels 7; Gaps 2;

QY      4 GPRPGAPCRAGPTI-----VLTSGRRQTLTSHGSSSPARATLGKPLV 45
      ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      492 GPRPAAAAAATPAVRTVPQKYAAGVRNPQQHLNAQP-QVTMQQPAV 538

RESULT 23
US-10-821-234-1168
; Sequence 1168, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1168
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1168

Query Match      18.7%; Score 50; DB 6; Length 529;
Best Local Similarity 29.2%; Pred. No. 39;
Matches 21; Conservative 6; Mismatches 25; Indels 20; Gaps 2;

QY      1 MAAGPR-PGAPCRAGPTIVLTSGRRQTL-----SHGSSSPARATL 40
      : ||||| | | | | | | | | | | | | | | | | | | | | |
Db      5 LLAGPRLPGVPGPAGAQSMAGAGPKRRALAAPAAEKEEREKMLAKSADGSAPAGEGE 64

QY      41 GKPLVLNDYSLN 52
      | | | | | | | |
Db      65 GVTLQRNITLLN 76

RESULT 24
US-10-131-826A-10
; Sequence 10, Application US/10131826A
; Publication No. US20050245730A1
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```
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-10

Query Match      18.7%; Score 50; DB 6; Length 594;
Best Local Similarity 37.8%; Pred. No. 45;
Matches 14; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY      3 AGPRPGAPCRAGPTIVLTSGRRQTLTSHGSSSPARAT 39
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      358 APPQPGGP----APGRNASARRRRSSSSSSSSASRTS 390

RESULT 25
US-11-186-731-2
; Sequence 2, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047PIRCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
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; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/026233
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.
; SEQ ID NO 243
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-243

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Query Match	18.5%;	Score 49.5;	DB 7;	Length 1464;
Best Local Similarity	44.1%;	Pred. No. 1.5e+02;		
Matches 15; Conservative	4;	Mismatches 12;	Indels 3;	Gaps 2;
OY	3	AGPRPGAPCRAGAPTIVLTSGRRQTLSHGSSSPA	36	
			:	:
Db	1042	AGP-PGAPGPAGPGVCPAGK--SGDRGETGA	1072	
			:	:

RESULT 34
US-11-186-284-28
; Sequence 28, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-28

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Db      1042 AGP-PGAPGAPGAPGVGPAGK--SGDRGETGPA 1072

RESULT 35
US-10-821-234-1096
; Sequence 1096, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1096
; LENGTH: 1467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1096

Query Match          18.5%; Score 49.5; DB 6; Length 1467;
Best Local Similarity 44.1%; Pred. No. 1.5e+02;
Matches 15; Conservative 4; Mismatches 12; Indels 3; Gaps

QY      3   AGPRPGACPCRAGAPTIVLTSGRRQTLSHGSSSPA 36
        ||| |||| | | | | : | : | |
Db      1045 AGP-PGAPGAPGAPGVGPAGK--SGDRGETGPA 1075

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RESULT 36
US-10-995-561-988
; Sequence 988, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 988
; LENGTH: 1823
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-988

Query Match      18.5%;      Score 49.5;      DB 6;      Length 1823;
Best Local Similarity 39.5%;      Pred. No. 1.9e+02;
Matches 15;      Conservative 3;      Mismatches 15;      Indels 5;      Gaps 2;

Qy      5      PRPGAPCRAGAPTIVLTSGRRQTLSHGS--SSPARATL 40
      |||      |||      |      |      |      |      |      |      |
Db      225      PTPGV---AAATLVGGGGTSSSTSSGSFEASVPEPOL 259

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RESULT 37
US-10-995-561-990
; Sequence 990, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 990
; LENGTH: 2102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-990

Query Match 18.5%; Score 49.5; DB 6; Length 2102;
Best Local Similarity 39.5%; Pred. No. 2.2e+02;
Matches 15; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

Qy 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGS--SSPARATL 40
Db 504 PTPGV---AAAPTLVSGGSTSTSSGSFEASPVPEPQL 538

RESULT 38
US-10-995-561-989
; Sequence 989, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 989
; LENGTH: 2108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-989

Query Match 18.5%; Score 49.5; DB 6; Length 2108;
Best Local Similarity 39.5%; Pred. No. 2.2e+02;
Matches 15; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

Qy 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGS--SSPARATL 40
Db 504 PTPGV---AAAPTLVSGGSTSTSSGSFEASPVPEPQL 538

RESULT 39
US-10-995-561-991
; Sequence 991, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 991
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-991

Query Match 18.5%; Score 49.5; DB 6; Length 2157;
Best Local Similarity 39.5%; Pred. No. 2.3e+02;
Matches 15; Conservative 3; Mismatches 15; Indels 5; Gaps 2;

Qy 5 PRPGAPCRAGAPTIVLTSGRRQTLSHGS--SSPARATL 40
Db 559 PTPGV---AAAPTLVSGGSTSTSSGSFEASPVPEPQL 593

RESULT 40
US-11-186-284-26
; Sequence 26, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 3063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-26

Query Match 18.5%; Score 49.5; DB 7; Length 3063;
Best Local Similarity 36.8%; Pred. No. 3.4e+02;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 2 AAGPR--PGAPCRAGAPTIVLTSGR-RQTLSHGSSSPA 36
Db 2849 AMGPRGPPGRPGSPGPGTGTGPGKPGKPGDHRPGPS 2886

RESULT 41
US-10-995-561-1014
; Sequence 1014, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1014

Query Match 18.3%; Score 49; DB 6; Length 407;
Best Local Similarity 35.4%; Pred. No. 39;
Matches 17; Conservative 8; Mismatches 13; Indels 10; Gaps 3;

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